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Listing first 45 summaries
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2: gb_htg:*
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Gapop 10.0 , Gapext 1.0
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10417.263 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

TITLE

Ramanathan,C., Feder,J., Nelson,T., Cacace,A., Barber,L. and Rysek,R.P.
A novel human g-protein coupled receptor, hgprbmy23, expressed

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

AUTH	REFERENCE	SOURCE	LOCUS DEFINITION ACCESSION VERSION VERSION	RESULT	4.4 4.10	0 C	- A- (3 G 7 T	ω u.	i w i		30	228	27	2 22 1	ມຸນ	22	ı Kı	c 19	c 17		14	12	1.	۱۵ ۵		љ и	n a-u			ö	
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/evidence=not_experimental
/product="seven transmembrane helix receptor"
/protein_id="BAC06095.1"
/db_xref="GI:21929019"
/translation="MNEPLDYLANASDFPDYAAAFGNCTDENIFLKMHYLPVIYGIIF
LVGFPGNAVVISTYIFKNRPWKSSTIINLNLACTDLLYLTSLEFLIHYYASGENWIFG
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AX379470
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Isolated human g-protein coupled receptors, nucleic encoding human gpcr proteins, and uses thereof Patent: WO 0187980-A 3 22-NOV-2001;
Applera Corporation Robert A. Millman Assistant Secrical Conference of the confer
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 15655)
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Federspiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Lam,B., Marathe,R., Miranda,M., Morehouse,A.J., Nguyen,M.
Oefner,P., Palm,C.J., Ramirez,D., Southwick,A.M., Wilhelmy,J.,
Yu,S. and Davis,R.W.
                                                                                                                                                                                          Homo sapiens chromosome 13 clone AC026756
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                                     GACCTTGGAAGAGCAGCATCATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATC
                                                                         GACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATC
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                                                                                                                                    TCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTTTCAAAATGA
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Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federspiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Mao, J., Marathe, R., Morehouse, A.J., Oefner, P., Palm, C.J., Mao, J., Marathe, R., Morehouse, A.J., Oefner, P., Palm, C.J., Ramirez, D., Wilhelmy, J., Yu, S. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
On Feb 23, 2001 this sequence version replaced gi:12745089
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Submitted (23-FEB-2001) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: hum-info@sequence.stanford.edu
------ Project Information
Center project name: 870
Center clone name: RP11-286P8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Stanford
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/clone_lib="RPCI human BAC library
30845 c 30755 g 46207 t
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|db_xref="taxon:9606"
|chromosome="13"
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100.0%; Pred. No. 1e-270;
tive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hampe, W
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1 (bases 1 to 1092)
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/db_xref="GI:21728284"
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TTIIHTLTHGLQTDSCLKQKARRITILLLLAFYVCFLPFHIRVIRIESRLLSISCSI
                                          enqiheayivsrplaalntfgnlllyvvvsdnfqqavcstvrckvsgnleqakkisys
                                                                                                                                                                                                                      gene="GPR99"
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           TCAACAGTGAGATGCAAAGTAAGCGGGAACCTTGAGCAAAGCAAAGAAAATTAGTTACTCA
                                                                            ACCTTTGGTAACCTGTTACTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGC
                                                                                                                                       TCCATTGAGAATCAGATCCATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAAC
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                                                                                                                 TCCATTGAGAATCAGATCCATGAAGCTTACATCGTT
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Pred. No. 1.2e-261;
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Sequence
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                                    Ramakrishnan,S.

Regulation of human p2yl-like g protein-coupled Patent: WO 0214511-A 5 21-FEB-2002;
                                                                                    Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                             CTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAA 1013
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                                                            CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACCTGTTA
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Pred. No. 2.7e-253;
0; Mismatches 0;
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/product="g protein-coupled receptor"
/product="g protein-coupled receptor"
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/protein_id="AAL26480.1"
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LVGFFGNAVVISTYLIKMRPWKSSTIINLNIACTDLLYLTSLEFFLHYYXASGENWIFG
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SLVAVIPMTFLITSTMRTNRSACLDLTSSDELATIKMYNLILTATTFCLPLVIVTLCY
TTIHTLTHGLQTDSCLKQKARRLTILLLLAFYVCFLFFHILRVIRIESRLLSISCSI
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  GCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACT
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Patent: WO 0187937-A 10 22-NOV-2001;
Incyte Genomics, Inc. (US)
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/db_xref="taxon:9606"
/note="Incyte ID No: 6575963CB1"
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Butheria; Primates; Catarrhini; Hominidae; Homo.
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ATTICACTGGTAGCTGTCATTCCGATGACCTTCTTGATCACATCAACCAGCAGCAAC 590	AGCTGCTTTTCCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTTGGTGTGGATC 530	AGCATCCTCTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATG 470	ATCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGC 410	CTGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGGGAAAACTGG 350	TTCAAAATGAGAACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGAT 290 	TATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATT 230 	GCTTTTGGAAATTGCACTGATGAAAACATCCCACTCAAGATGCACTACCTCCCTGTTATT 170 	ACCATGAATGAGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCCGATTATGCAGCT 110	Query Match 90.7%; Score 980.8; DB 6; Length 1020; Best Local Similarity 99.5%; Pred. No. 1.2e-244; Matches 1015; Conservative 0; Mismatches 2; Indels 3; Gaps 3;	/organism="romo sapiens" /db_xref="taxon:9606" 261 a	Novel g protein-coupled receptors AL Patent: WO 0136473-A 85 25-MAY-2001; PHARMACIA & UPJOHN COMPANY (US) S Location/qualifiers 1. 1020	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom 1 (bases 1 to 1020) 1 (bases 1 to 1020) Vogeli,G., Wood,L.S., Parodi,L.A., Hiebsch,R.R., Lind,P. Slightom,J., Schellin,K.A., Kaytes,P.S., Bannigan,C.M., Sejlitz,T. and Huff,R.M.	AX147840 AX147840.1 GI:14346841 human. Homo sapiens Hokaryota: Metazoa: Chordata: Craniata: Vortebrata: Enteleos		GTAAGCGGGAACCTTGAGCAAAGAAAAATTAGTTACTCAAACAACCCTTGA 1067 	

Search completed: January 30, 2003, 10:36:21 Job time: 3480 secs

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Result
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RESULT 1
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XX Homo
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ALIGNMENTS

Bruess M, 22-SEP-2000; 2000DE-1046970. 22-SEP-2000; 2000DE-1046970. 11-APR-2002. DE10046970-A1 Homo sapiens. Human; P2Y1-li; chromosome 13; G protein-coupled; receptor; gene therapy; thyroid; ds. (BRUE/) BRUESS M. (BOEN/) BOENISCH H. Boenisch H; Location/Qualifiers 3188..4201 /product= "P2y1-like purine receptor"

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P-PSDB; AA014027.
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Novel isolated G-protein coupled receptor peptide useful for treating disorder characterised by absence of, in appropriate or unwanted expression of the receptor protein, and as immunogens to raise antibodies

Claim 23; Fig 3; 64pp; English.

The present specifically claimed human genomic DNA sequence (located on chromosome 13) encodes a purinergic-related G-protein coupled receptor (GPCR) of the invention. GPCRs constitute a major class of proteins responsible for signal transduction within a cell. Upon binding of a ligand to the extracellular portion of a GPCR, a signal is transduced resulting in a biological or physiological change within the cell. The GPCR proteins can be divided into five families, family I contains the purinergic GPCRs (e.g. the P2Y receptors). P2Y receptors are characterised by their selective responsiveness towards ATP and its analogues, some also respond to UTP. The invention comprises a human G-protein coupled receptor protein and encoding nucleic acids. The GPCR protein and nucleic acids of the invention are useful in the treatment of a disease or condition mediated by a human protease. The GPCR protein of the invention is useful for the development/identification of therapeutic proteins; assays designed to quantitatively determine levels of the protein in biological fluids; identifying compounds which modulate the activity of the GPCR, or the interaction of the GPCR and a molecule with which it normally interacts; and treating a disorder characterised by an absence of, or inappropriate expression of the GPCR protein. The GPCR nucleic acids of the invention are useful in: diagnostic assays to identify changes in the GPCR nucleic acid that lead to pathology; controlling GPCR expression; and in gene therapy to treat patients with aberrant GPCR gene expression. The GPCR nucleic acids can also be used in the production of transgenic animals.

Sequence 9905 BP; 2656 A; 2218 C; 2061 G; 2970 T; 0 other;

В 8 S В S 밁 S В 밁 밁 8 ঠ 밁 Ś S Query Match 100.0%; Best Local Similarity 100.0%; Matches 1081; Conservative 0; 8496 8556 8316 8256 CATATTGCCAAACTGAACTCTCTTGTTTTCTTGCAAGATGAAAGGAGACAACCATGAATG 8616 8436 8376 361 301 481 CCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGGATCATTTCACTGG 540 241 121 13 1 TCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGAGCTGCTTTT 480 GACCTTGGAAGAGCAGCATCATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATC TCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGAGCTGCTTTT ATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCACTTCAACCTGTATAGCAGCATCCTCT ATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCT 420 TGACCAGCCTCCCCTTCCTGATTCACTATGCCAGTGGCGAAAACTGGATCTTTGGAG TGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAACTGGATCTTTGGAG 360 GACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATC 300 TCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTTACATTTTCAAAATGA 8495 TCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTTTCAAAATGA 240 AGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCGATTATGCAGCTGCTTTTGGAA AGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCCGATTATGCAGCTGCTTTTGGAA 120 CATATTGCCAAACTGAACTCTCTTGTTTTCTTGCAAGATGAAAGGAGACAACCATGAATG 60 Score 1081; DB 24; Pred. No. 1.9e-306; 0; Mismatches 0; Indels Length 9905; 0; Gaps 8735 8675 . 8375 8615 8555 8315

9336 C 9336	뭣
1081 C 1081	Ş
9276 GGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAACAACCCTTGAAATATTTCATTTA 9335	B
1021 GGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAACAACCCTTGAAATATTTCATTTA 1080	Ş
9216 TGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAAGTAAGCG 9275	Db
961 TGGTCGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAAGTAAGCG 1020	Ś
9156 CTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACCTGTTACTATATG 9215	망
901 CTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTTGGTAAACCTGTTACTATATG 960	Ş
9096 TTCGGATCGATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATCCATGAAG 9155	뮰
841 TTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATCCATGAAG 900	Ş
9036 CCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTACCCTTCCATATCTTGAGGGTCA 9095	DЬ
781 CCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTTTACCCTTCCATATCTTGAGGGTCA 840	Ş
8976 ACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGCTAA 9035	문
721 ACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGCTAA 780	8
8916 CTGCAACTACTTTCTGCCCTCCCCTTGGTGATAGTGACACTTTGCTATACCACGATTATCC 8975	ઠ
661 CTGCAACTACTTTCTGCCCCCCTTGGTGATAGTGACACTTTTGCTATACCACGATTATCC 720	Ş
8856 GTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTGATTTTGA 8915	밁
601 GTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTGATTTTGA 660	S
8796 TAGCTGTCATTCCGATGACCTTCTTGATCACATCAACCCAACAGGACCAACAGATCAGCCT 8855	망
541 TAGCTGTCATTCCGATGACCTTCTTGATCACCTAACCAACAGGACCAACAGATCAGCCT 600	Ş
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RESULT 3

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AAS08362 standard; cDNA; 1729 ВP

26-SEP-2001 (first entry)

Human cDNA encoding G-protein coupled receptor, GPCR 39404.

AASO8362
ID AASO
XX AASO
XX 26-S
XX 26-S
XX Huma
XX Huma
XX Huma
XX Huma
XX Huma
XX Homc
XX Hom
XX Hom Good pasture's syndrome; viral hepatitis; Alzheimer's disease; lymphoma; Heymann nephritis; Paget's disease; Crohn's disease; endometriosis; systemic lupus erythematosus; actinic keratosis; myocarditis; Kawasaki syndrome; DiGeorge syndrome; peripheral B-cell neoplasm; inflammations; teratoma; ss. Human; G-protein coupled receptor; GPCR; 39404; immunogen; antibody;

Homo sapiens.

Location/Qualifiers 294..1307 /*tag= a /product= "Protein 39404"

WO200149847-A2

12-JUL-2001.

22-DEC-2000; 2000WO-US35309.

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Best Local Similarity
Matches 1080; Conserv
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
661
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         TCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGAGCTGCTTTT
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25-MAY-2000;
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18-JUL-2000;
13-DEC-2000;
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Best Local Similarity
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(a) assessing whether a patient is affilicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prostate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; prostate cancer;
pharmacogenomic marker;
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Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -Page 6487-6488; 11750pp; English

WPI;

2001-662795/76.

The invention relates to an isolated nucleic acid molecule (I) a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) o) comprising of the

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CAACAGTGAGATGCAAAGTAAGCGGGAACCTTGAGCAAAGCAAAGAAAATTAGTTACTCAA
                                            CCTTTGGTAACCTGTTACTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCT
                                                                                 CCATTGAGAATCAGATCCATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACA
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                                                                                                                                        TACCCTTCCATATCTTGAGGGTCATTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTT
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21-AUG-2000;
26-SEP-2000;
26-SEP-2000;
                                                                                                                                        Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents -
                                                                                                                                                                                                                                                              WPI; 2001-355616/37.
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11-FEB-2000;
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23-DEC-1999
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/product= "hRUP21"
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The sequence encodes a human G-protein coupled receptor (GPCR), hRUP21 The endogenous and non-endogenous, constitutively activated versions of human G-protein coupled receptors (GPCR), are useful for direct identification of candidate compounds as receptor agonists,

for

Claim 55;

Page 113-114; 159pp;

English

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                                                                          CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACCTGTTA
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05-JUN-2002 ABK11381; ABK11381 standard; DNA; 1014 (first entry. ВP

Human DNA encoding P2Y1-like G protein-coupled receptor

Human; ds; gene; P2Y1-like G protein-coupled receptor; GPCR; infection; pain; cancer; anorexia; bullmia; asthma; hypotension; central nervous system disease; acute heart failure; hypertension; urinary retention; osteoporosis; diabetes; angina pectoris; myocardial infarction; ulcer; inflammation; allergy; multiple sclerosis; benign prostatic hypertrophy; psychosis; neurological disorder; dyskinesia; HIV; human immunodeficiency virus infection; CNS disorder; Parkinson's disease; anxiety; schizophrenia; manic depression; dementia; severe mental retardation; Huntington's disease; lourette's syndrome.

sapiens

WO200214511-A2 /*tag= /*tag= a /product= "P2Y1-like 1..1014 Location/Qualifiers

21-FEB-2002.

10-AUG-2001; 2001WO-EP09243

14-AUG-2000; 2000US-224989P

(FARB) BAYER

Ramakrishnan

2002-257607/30.

asthma, Novel human P2Y1-like G protein-coupled receptor polypeptide which can be regulated for treating infection, pain, cancer, diabetes, anorexia, hypertension, neurological disorder and dyskinesia

Claim 1; Fig 5; 118pp; English

CC receptor (GPCR) polypeptide and the nucleic acids encouring a conceptor (GPCR) polypeptide and the nucleic acids encouring a conceptor (GPCR) polypeptide and as sequences, promoters, fragments, variants, or a conceptor (GPCR) and 3 sequences, promoters, fragments, variants, or a sequence encoding a protein at least 50% identical to the GPCR).

CC Also included are an expression vector comprising the nucleic acid, conception and the identification of modulators of the GPCR each of a suspension vector and the identification of modulators of the GPCR and is useful for detecting a polymucleotide encoding the GPCR in a biological sample. The GPCR and nucleic acid are useful for for modulators of the GPCR. The modulator or agent useful for modulators of the GPCR. The modulator or agent useful for modulating contral for modulators of the GPCR. The modulator or agent useful for modulating bacterial, fungal, protozoan, and viral infection, pain, cancer.

CC anorexia, bulimia, asthma, central nervous system (CNS) disease, acute bacterial fungal, protosoan, and viral infection, pain, cancer, acute costeoporosis, diabettes, angina pectoris, mycardial infarction, ulcer, osteoporosis, diabettes, angina pectoris, benign prostatic hypertrophy, companied the protosoan of the GPCR. The section of the GPCR and neurological disorders, dyskinesias, HIV virus infection companied the contral infarction and peurological disorders such as parkinson's contral and contral protocons and prostatic hypertrophy, schizophrenia, manic depression, delirium, dementia, RESULT 11
ABK11381
AC ABK11
AX ABK11
ABK11
AX AB The invention relates to a purified human P2Y1-like G protein-coupled receptor (GPCR) polypeptide and the nucleic acids encoding it

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                                                 CTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAA 1013
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RESULT 13
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XX D4-OC
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XX Human
XX Human
XX Homo
XX AGA
XX EP121
XX EP122
XX 04-OCT-2002 ABQ78847; ABQ78847 standard; cDNA; (first entry) 1014 ₽P

Human; G-protein coupled receptor; GPCR; PFI-019; neuroprotective; anti-inflammatory; cytostatic; cardiovascular; antiallergic; hypotantiarteriosclerotic; osteopathic; hypertension; asthma; Human G-protein coupled receptor artherosclerosis; gene; ss. PFI-019 CDNA

sapiens

EP1219638-A2 /*tag= a /product= Location/Qualifiers
1..1014 "PFI-019"

04-DEC-2001; 2001EP-0310136

03-JUL-2002.

18-DEC-2000; 2000GB-0030854. 04-MAY-2001; 2001GB-0011031.

(PFIZ) PFIZER LTD. PFIZER INC.

Fidock MD;

WPI; 2002-521945/56. P-PSDB; ABB81902.

New G-protein coupled receptor (GPCR) polypeptide with homology to P2Y purinoreceptor, useful for treating e.g. inflammation or cancers in a patient, or for screening GPCR agonists or antagonists for treating diseases

Claim 1; Page 12; 19pp; English

The invention relates to a novel G-protein coupled receptor (GPCR), and the polynucleotide encoding it. The protein of the invention has neuroprotective, anti-inflammatory, cytoscatic, cardiovascular, antiallergic, hypotensive, antiarteriosclerotic, and osteopathic activity. The GPCR polypeptide is useful for manufacturing a medicament for treating a patient who needs to upregulate a receptor. Preferably, therapeutically useful areas are hypertension, asthma, and artherosclerosis. The sequence encodes the G-protein coupled receptor of the invention, PFI-019.

Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 other;

N/C

밁 Ś 뭉 Ś Query Match 93.7 Best Local Similarity 99.9 Matches 1013; Conservative 114 61 54 ATGAATGAGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCGATTATGCAGCTGCT 113 93.7%; 99.9%; Score 1012.4; Pred. No. 8.5e 0; Mismatches <u>,</u> .5e-287; DB 24; Indels Length 1014; .. Gaps 60 0,

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XW Addir

26-MAR-2002 AAD26370

(first entry)

AAD26370 standard;

CDNA; 1014

ВP

Human G-protein coupled receptor 2

(GCREC-2) cDNA.

atherosclerosis; hypertension; myocardial infarction; peptic ulcer; gastrointestinal disorder; dysphagia; anorexia; autoimmune disorder; acquired immune deficiency syndrome; inflammator disorder; infection addison's disease; allergy; Grave's disease; metabolic disorder. Anno Addison's disease; allergy; Grave's disease; metabolic disorder.

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54 ATGAATGAGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCCGATTATGCAGCTGCT

Query Match Best Local s

93.7**%**;

Score 1012.4; Pred. No. 8.5e 0; Mismatches

8.5e-287;

DB 24;

Length

1014;

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Gaps

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Sequence 1014

BP;

259 A; 263 C; 188 G;

304 T; 0 other

emphysems, Grave's disease, gout, multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus, uveitis, viral, bacterial, fungal, parasitic, protozoal and helminthic infections and trauma, metabolic disorders such as diabetes, obesity and osteoporosis; and viral infections such as infection caused by viral agent classified a adenovirus, arenavirus, bunyavirus. Polynucleotides of the invention are useful as probes for assessing toxicity of test compounds. They a also used in gene therapy. The present sequence is human G-protein coupled receptor 2 (GCREC-2) cDNA.

are as

Best Local Similarity Matches 1013; Conserv

Human; G-protein coupled receptor 2; cell proliferative disorder; arteriosclerosis; hepatitis; cancer; neurological disorder; epilepsy; Alzheimer's disease; Parkinson's disease; cardiovascular disorder;

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Parkinson's disease, ataxias, multiple sclerosis, bacterial and viral meningitis, Creutzfeldt-Jakob disease, schizophrenic disorders, amnesia; cardiovascular disorders such as arteriovenous fistula, atherosclerosis, hypertension, vascular tumours, myocardial infarction, hypertensive heart disease, infective endocarditis, cardiomyopathy, myocarditis; gastrointestinal disorders such as dysphagia, peptic oesophagitis, emesis, anorexia, nausea, peptic ulcer, choleithiasis, diarrhoea, constipation, acquired immune deficiency syndrome (AIDS), hepatic encephalopathy; autoimmune/inflammatory disorders such as Addison's disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact dermatitis, Crohn's disease, diabetes mellitus, Goodpasthres's syndrome, amburgema Grave's Aicasaac cout multiple sclerosis syndrome, semborada character and semborada contact multiple sclerosis syndrome.
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22-MAY-2000;
25-MAY-2000;
02-JUN-2000;
02-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human G-protein coupled receptor (GCREC) polypeptides and polynucleotides. GCREC polypeptides are useful for screening compounds that modulate their activity. They are useful in the diagnosts, prevention and treatment of disorders which include cell proliferative disorders such as arteriosclerosis, hepatitis, myelofibrosis, psoriasis and cancer including adenocarcinoma, leuka
                                                                                                                                                                                                                                                                                                                                                                                     lymphoma; neurological disorders such as epilepsy, ischaemic cerebrovascular disease, Alzheimer's disease, Pick's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel G-protein coupled receptors and polynucleotides useful for diagnosis, treatment and prevention of disorders of cell proliferation, neurological, cardiovascular, metabolic disorders and viral infections
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Hafalia A;
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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108.8	109.4	114.6	115.6	126.6	257	Score
10.1	10.1	10.6	10.7	11.7		Query Match
663	877	638	641	623	744	Query Match Length DB
13	12	9	14	14	14	: B
BM426517	BG402029	AL675845	BQ396255	BQ038875	BM723768	Length DB ID
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CNS04VV3	BQ724793	BG579061	BE627479	AA177828	BC027965	BM918711	AL546894	AL545172	BI837965	BM008116	BG914321	BM258063	BQ396804	BE314834	BQ959110	CNS045P5	BI768397	AL521440	BQ897419	AL836006	BQ551383	AL520218	BI819396	AL525099	BB864882	BM918491	BI401676	BB660768	BI833118	AZ953874	BG924078	BB847918	AK005013	AK017378	AI663305	AL588350	BG712193	CNS0532S
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ALIGNMENTS

	MEDLINE COMMENT	TITLE	REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BM723768 LOCUS DBFINITION
Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA 761: 319 335 8250 Fax: 319 335 9565 Email: mSodreS@blue.Weeg.uiOWd.edu Tissue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa	cenome wes. 6 (3), /31-806 (1398) 97044477 Contact: Soares, MB	Normalization and subtraction: two approaches to facilitate gene discovery	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 74) Bonaldo, M.F., Lennon, G. and Soares, M.B.	BM723768.1 GI:19045099 EST human. Homo sapiens	BM723768 744 bp mRNA linear EST 01-MAR-2002 UI-E-E01-aix-g-16-0-UI-E-E01 Homo sapiens cDNA clone

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 TTGTTACCACCAGTTCCAATGGGGACAGCACCACCTGCCATGACACTTCCAGCGTGGATC
                                    TGATCACATCAACCAACAGGACCAACAGATCAGCCTGTCTCGACCTCACCAGTTCGGATG
                                                                      GGATTATTTCCGTGGTCGGCTGGGTTATCGTTTCCGCCTGTCAGTCCCCTATATTGTACT
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intram
Sequencing Center (NISC)
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National Institute of Child Health and Human Development, National
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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/dev_stage="embryo, stages 14-19"
/lab_host="DHIOB (phage-resistant)"
/note="Vector: pCMV-SPORT6.ccdb; Site_1: NotI; Site_2:
EcoRV; Cloned unidirectionally. Primer: Oligo dT. Average
insert size 2.1 kb. Constructed by Invitrogen. Note: This
is a Xenopus Gene Collection (XGC) library."
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                                                            TCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCTTCCTCACCTGTTTCAGCATCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taylor,R., Ashurst,J.L., C
Sanger Xenopus tropicalis
Unpublished (2001)
Contact: Taylor R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL675845 XGC-gastrula Silurana tropicalis cDNA clone TGas051n19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is from a Xenopus Gene Collection constructed by Aaron M. Zorn.
Location/Qualifiers
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hinxton,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev stage="gastrula (stages 10.5-13 mixed)"
/lab host="Escherichia coli XII-blue"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:8364"
/clone="TGas051n19"
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Pred. No. 8.8e-22;
0; Mismatches 245
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Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fishe Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

Estimate of human gene number provided by genome-wide analy, using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALI18925.1 GI:9551809
GSS; genome survey sequence.
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Neoteleostei;
Accinopterygii; Neopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                 This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                Bernot, A. and Weissenbach, J.

Characterization and repeat analysis of the compact freshwater pufferish Tetraodon nigroviridis
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/note="Genoscope sequence ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTACGTGGGCATCTGCCACCCGATTAAGGCGCTGAATCTGGTGAANCCCCCGANATTCCT 152
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                                                                                                                                                                                                    Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 491 bp mRNA linear EST 08-MAY-2001 pglln.pk011.f3 Normalized Liver Library Gallus gallus cDNA clone pglln.pk011.f3 5' similar to gblpAAC60339.1 (AF031897) G protein coupled P2Y nucleotide receptor [Meleagris gallopavo]G, mRNA
                                                                                                                                                                                                                                                                         Burnside, J., Morgan, R.W. and Conchicken BSTs from a normalized Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasian: Phasianinae; Gallus.
                                                                                                                                                                          Tel: 302 831-1345
Fax: 302-831-3411
                                                                                                                                                                                                                                                            Contact: Joan Burnside
                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                   chicken.
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                                                                                                                                                                                                                                                                                                                          (bases 1 to 491)
                                                                                                                                     joan@UDel.Edu, www.chickest.udel.edu
Location/Qualifiers
                                 /clone_lib="Normalized Liver
/sex="Male and Female"
'tissue_type="liver"
'lab_host="E.coli EM
                                                                  clone="pglln.pk011.f3"
                                                                                      db_xref="taxon:9031"
                                                                                                     organism="Gallus gallus"
                                                                                                                         . 491
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Pred. No. 1.3e-19;
0; Mismatches 216;
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alized liver library
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                                                                                                      PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCATGCTCTTGCTCACTGTCATTATCATGGACCGATATCTGCTCATGAAGTACCCTGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238;
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to
                                                                                                                                               Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                         HTC; CAP trapper.

Mus musculus (strain:C57BL/6J) 6 days neonate head cDNA to clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                       2542 bp mRNA linear HTC 19-JAN-200 Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430432015:purinergic receptor P2Y, G-protein coupled 2, full insert sequence.

AK017378
                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                            Mammalia;
                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                               clone:5430432J15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
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                                                                                                                                                                                                                                          Eutheria;
                                                                                                                                                                                                                                                                Metazoa;
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Pred. No. 3.4e-18;
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8 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Adachi, J., Aizawa, K., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Arakawa, T., Baldarelli, R., Bono, H., Furuno, M., Hanagaki, T., Arakawa, T., Baldarelli, R., Bono, H., Furuno, M., Hanagaki, T., Hori, F., Hiracka, T., Hori, F., Hiracka, T., Hori, F., Hiracka, T., Hori, F., Hime, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Koya, S., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Salto, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, X., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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                                                                                                                                                                                                                                                                                                                                     Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Plans B1-45-503-9216)
                                                                                                               cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rigenomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409 (6821), 685-690 21085660
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    Division of Experimental Animal Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayashizaki,Y.
                                                                                                                                                                                                                                                                 Please visit our web site (http://genome.gsc.riken.go.jp/) further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Please visit our web site (http://genome.gsc.riken.go.jp/)
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         630
/gene="P2ry2"
/note="putative"
a 861 c 834
                                                                                                                                                                                                                                        TVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRFLHSLRWGRARYARRVAAVVWVL
VLACQAPVLYFVTTSVRGTRITCHDTSARELFSHFVAYSSSWLGLLFAVPFSVILVCY
VLMARRLLKFAYGTTGCLFRAKRKSVRZTIALVLAVFALCFLPFHLTRTLYSSRSLDL
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VLGLCLNVVALYIFLCRLKTWNASTTYMFHLAVSDSLYAASLPLLVYYYARGDHWPFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         purinergic receptor P2Y, G-protein coupled 2
putative"
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477. .1598
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                                                                                                                                                         gene="P2ry2"
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|clone_lib="RIMEN full-length enriched mouse cDNA library"
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clone="1300015C04"
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'db_xref="MGD:MGT:1895057"
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N.,
                                                                                                                                                                                                                                                                      Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jag
                                                                                                                                                                                                                                     Unpublished (2001)
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                                                                                                 1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                              Contact: Yoshihide Hayashizaki
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                            Fax: 81-45-503-9216
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  Sugahara, Y.,
                                                                                                                    Kanagawa 230-0045, Japan
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0219 row: L column: 17
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gli4732114 [gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant very. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0219L17"
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GCTGCCACATGCATCCATCGCAACCGCACTGTGTGCTACGACCTGAGC 507
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-559-524A-1
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                                                                                        Matches 380;
                                                                                                                     Query Match
Best Local Similarity
108 GCTGCTTTTGGAAATTGCACTGATGAAAACATCCCACTCAAGATGCACTACCTCCCTGTT 167
                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
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ALIGNMENTS	PCT-US94-06380-2	00-09-10#+290-3	TTG-09-104 200 2	US-08-801-228-3	US-08-801-238-3	US-08-802-627A-3	US-08-805-478-3	US-08-284-586-3	US-08-701-265-3	US-08-076-093A-3	US-08-202-056-4	US-U9-51/-6U5-14	100 00 F13 COT 14	US-09-582-224A-5	PCT-US93-11153-45	US-09-088-337B-45	US-09-299-843A-45	US-08-153-848-45	US-08-742-440A-1		PCT-11895-07180-1	
	Sequence 2, Appli	sequence 3, Appli	-	u (ω.	ω	Sequence 3, Appli	w.	ω		Sequence 4, Appli	Sequence 14, Appl	TINGE 'C DOTTONDO	ח ל	5	45		45,	Sequence 1, Appli	reductive t' voltan		

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Sequence 1, Application US/08559524A Patent No. 5871963
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 202-467-7000
                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEB: MORGAN, LEWIS &
STREET: 1800 M Street, N.W.
                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                           TYPE: STRANDEDNESS: 814,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0
FILING DATE: 15-NOV-1995
CLASSIFICATION: 435
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NOVEL PURINERGIC RECEPTOR
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Score 129; DB 2;
Pred. NO. 1.4e-29;
0; Mismatches 370;
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US-08-442-134A-
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Best Local Similarity
Matches 222; Conserv
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INFORMATION FOR SEQ ID NO:
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LENGTH: 1842 base pair
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
      282
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ATTORNEY/AGENT INFORMATION:
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                                                                                         219 TCCACTTACATTTTCAAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTG 278
                                                                                                                       159 CTCCCTGTTATTŢĄTGGCAŢTAŢCŢTCCTCGTGGGATŢTCCAGGCĄĄTGCĄGŢĄGTGAŢA 218
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LOCATION:
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TOPOLOGY: lin
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REGISTRATION NUMBER: 31.
REFERENCE/DOCKET NUMBER:
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GCTGTGTCTGATGCACTGTATGCGGCCTCCCTGCCGCTGCTGGTCTATTACTACGCCCGC
                           GCCTGCACAGATCTGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGT 338
                                                              TACATCTTCTTGTGCCGCCTCAAGACCTGGAATGCGTCCACCACATATATGTTCCACCTG
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No. 5596088th Carolina
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Post Office Drawer 34009
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VENTION: DNA Encoding the Human P2U Receptor and VENTION: Null Cells Expressing P2U Receptors
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Harden, Thomas K.
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                                                                                                                                                                                Score 103.2; DB 1;
Pred. No. 1.1e-21;
0; Mismatches 198;
                                                                                                                                                                                                               Length 1842;
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US-08-444-581B-1
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US-08-444-581B-1
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                                                                                                                                                                                     NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0
FILING DATE: 16-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                              FEATURE:
                                                                                MOLECULE TYPE:
                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                          LENGTH: 1842 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                    NAME: Sibley, Kenneth REGISTRATION NUMBER: 3
                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 19-MAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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No. 5607836th Carolina
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INVENTION: DNA Enc
                                                                                                                                                                                                              919-881-3175
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                 57..1181
                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thomas K.
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Best Local Similarity

9.5%;

Score 103.2; DB 1; Pred. No. 1.1e-21;

Length 1842;

Query Match

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION NUMBER: JP 6-
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PRIOR APPLICATION DATA:
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567 ATCACATCAACCAACAGGACCAACAGATCAGCCTGTCTCGACCTCACC 614
                                                                                                          376 CTGGGCATCTGCCACCCCTGGCTTCCTGGCACAAGCGTGGAGGTCGCCGTGCTGCTTGG 435
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                             450 TGTGTGATCATTCACCCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCAGTT--- 506
                                                                                                                                                                                      316
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                                                                                                                                                                                                                                                     256 TACGCCAGAGGGGACCACTGGCCCTTCGGAGACCTCGCCTGCCGCTTTGTACGCTTCCTC 315
                                                                                                                                                                                                                                                                                    330 TATGCCAGTGGCGAAAACTGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGC 389
                                                                                                                                                                                                                                                                                                                       196 CTGAACCTGGCACTGGCGGACCTGATGTATGCCTGTTCACTACCCCTACTTATCTATAAC 255
                                                                                                                                                                                                                                                                                                                                                           270 CTGAACCTGGCCTGCACAGATCTGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTAC 329
                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 200; Conserv
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                                    GTAGCCTGTGCTGTGGTGGATCATTTCACTGGTAGCTGTCATTCCGATGACCTTCTTG 566
                                                                                                                                                                             TTCTATGCCAATCTACATGGCAGCATCCTGTTCCTCACCTGCATTAGCTTCCAGCGCTAC 375
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                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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RESULT 7
US-08-513-974B-370
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                                                                                                                                                                                                                                                                                                                                                                                       PILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6
TELECOMMUNICATION INFORMATION:
                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: JP 6-
FILING DATE: 30-SEP-1994
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FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7.
FILING DATE: 16-MAR-1995
                                                                               ATTORNEY/AGENT INFORMATION:
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APPLICANT:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, ERONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
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                                     NAME: Resnick, David S
REGISTRATION NUMBER: 3:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  REFERENCE/DOCKET NUMBER:
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FILING DATE: 14-SEP-1995
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Ohgi, Kazuhiro
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Ohtaki, Tetsuya
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Best Local Similarity
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                                                                                                                                                            GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1475 base pair
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W.,
                                                                   APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 280
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
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APPLICATION NUMBER: US 08/390,301
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LOCATION:
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ilarity 52.6%;
Conservative
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Pred. No. 4.3e-20;
0; Mismatches 192;
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 Ste. 5500
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Best Local Sim.
Matches 213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
FEATURE:
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LENGTH: 1475 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: ADLER, REID G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 25-JAN-
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 887-0763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Wash:
STATE: D.C
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
GGCGTCTCCTTGGCAATCTGGCTCCTGATTTTTTCTGGTCACCATC 846
                                      GTTGTAGCCTGTGCTGTGTGTGGTATCATTTCACTGGTAGCTGTC 548
                                                                                                    CGCTACTGTGATCATTCACCCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCA
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                                                                    AGGTACTGGGTGATCGTGAACCCCCATGGGACACCCCCAGGAAGAAGGCCAAACATCGCCGTT
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Similarity 52.6%;
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Pred. No. 4.3e-20;
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RESULT 11 US-08-476-976-1

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US-08-486-673B-1
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Best Local Similarity 52.1
Matches 213; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 08/097,938
PRIOR FILING DATE: 1993-07-26
PRIOR APPLICATION NUMBER: PCT/US94/08536
PRIOR FILING DATE: 1994-07-26
NUMBER OF SEQ ID NOS: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Scarborough, Robert M.
TITLE OF INVENTION: Nucleic Acids Encoding the
FILE REFERENCE: 44481-5006-08-08
CURRENT APPLICATION NUMBER: US/08/486,673B
CURRENT FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sundelin, Johan
APPLICANT: Scarborough, R
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LOCATION: (232)..(1416)
OTHER INFORMATION: C140 recei
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ORGANISM: Mus musculus
FEATURE:
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                                                                                                                                                       324 CACTACTATECCAGTEGCGAAAACTEGATCTTTGGAGATTTCATGTGTAAGTTTATCCGC 383
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                                  GGCTTTTTCTATGGTAACATGTATTGCTCCATCCTCTTCATGACCTGCCTCAGCGTGCAG 741
                                                                         TTCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCTTCCTCACCTGTTTCAGCATCTTC 443
                                                                                                                    TCCTACCACCTACATGGCAACAACTGGGTCTACGGGGAGGCCCTGTGCAAGGTGCTCATT 681
CGCTACTGTGTGATCATTCACCCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCA 503
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Pred. No. 4.3e-20;
0; Mismatches 192;
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US-08-476-000-60
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30,988
REFERENCE/FOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
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324 CACTACTATGCCAGTGGCGAAAACTGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGC 383
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TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SUNDELIN, APPLICANT: SCARBOROU
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LOCATION:
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EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
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Copyright (c) 1993 - 2003 Compugen
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(cgn2 6/ptodata/1/pubpna/US06 NEW PUB.seq:*
(cgn2 6/ptodata/1/pubpna/US06 PUBCOMB.seq:*
(cgn2 6/ptodata/1/pubpna/US07 NEW PUB.seq:*
(cgn2 6/ptodata/1/pubpna/US07 NEW PUB.seq:*
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10 US-09-812-102-40

US-09-826-791-1

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10 US-09-788-133-1

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sequence 1, Appli
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CURRENT APPLICATION NUMBER: US/09/728,422
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 1
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NAME/KEY: CDS
LOCATION: (547)..(1239)
JS-09-728-422-1
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Best Local Sim
Matches 792;
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ACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGCTAA
                                                                      CTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCTATACCACGATTATCC
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Pred. No. 4e-221;
0; Mismatches 1;
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GENERAL INFORMATION:

APPLICANT: Robison, Keith B

TITLE OF INVENTION: NO. US20020055179A1e1 G-Protein Co.

FILE REPERENCE: 5800-41 035800/183478

CURRENT APPLICATION NUMBER: US/09/812,102

CURRENT FILING DATE: 2001-03-19

PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/09/812,102

PRIOR FILING DATE: 1999-07-30

NUMBER OF SEQ ID NOS: 90

SOFWMARE: PACENTIN Ver. 2.0

SOFWMARE: PACENTIN VER. 2.0
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Best Local Similarity
Matches 515; Conserv
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                        CTCCTTGCATTTTACGTATGTTTTTACCCTTCCA
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                                                                CATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGCTAACCATTCTGCTA
                                                                                             CATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGCTAACCATTCTGCTA
                                                                                                                                                                                                   ACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTGATTTTGACTGCAACTACT
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RESULT 5
US-09-826-791-1
; Sequence 1, Application US/09826791
; Patent No. US20010039037A1
; GENERAL INFORMATION:

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US-09-866-230-6
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Patent No. US20020150901A1
GENERAL INFORMATION:
APPLICANT: Murphy, Andrew, et al.
TITLE OF INVENTION: No. US20020150901A1el Nucleic Acids, Polypeptides, Methods of Mak
FILE REFERENCE: REG 771A
CURRENT APPLICATION NUMBER: US/09/866,230
CURRENT FILING DATE: 2001-05-25
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Best Local Similarity
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PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 9
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ORGANISM: Homo sapiens
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                             GGATCCTCTGTGGGATCATATGGATCCTTATCATGG 502
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                                                                                         GTTTCCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCT
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US-09-828-478-3
                                                                                                                                                                           GENERAL
                                                                                                                                                                                      Sequence 26, Application US/09728952 Patent No. US20020111302A1
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PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 16
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Local Similarity 52.3%;
nes 207; Conservarium
         OF INVENTION:
                                                                                                                                                                          INFORMATION:
                                                                              Liu, Chenghua
Asundi, Vinod
Wang, Jian-Rui
                                                                                                                         Tang, Y. Tom
Zhou, Ping
Goodrich, Ryle
                                               Wang, Dunrui
Yamazaki, Vicki
                                 Ujwal, Manusha L
       No.
Radoje T.
No. US20020111302A1el Nucleic Acids
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APPLICANT: Xiao, Yonghong
TITLE OF INVENTION: Regulation of Human CysLT2-Like
TITLE OF INVENTION: Protein
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CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR FILING DATE: 2000-04-07
719 GGATCCTCTGTGGGATCATATGGATCCTTATCATGG
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                                                                                           GTTTCCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCT
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                                                                                                                                              GCTACTGTGTGATCATTCACCCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCAG 504
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Pred. No. 1e-17;
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lee, James
APPLICANT: Wood, WIlliam I.
TITLE OF INVENTION: PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                 APPLICATION NUMBER: 1
FILING DATE: 24-June
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
              APPLICATION NUMBER: 08/70
PILING DATE: 22-AUG-1996
PRIOR APPLICATION DATA:
                                                                                                                                   SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
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   APPLICATION NUMBER:
                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                         CITY: South San Francisco
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49.8%;
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08/664228
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Pred. No. 8e-15;
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RESULT 14 US-09-962-832-218

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Sequence 218, Application US/09962832 Patent No. US20020110821A1

GENERAL INFORMATION:

APPLICANT: Ebner, Reinhard

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sig

TITLE OF INVENTION: Sets

FILE REFERENCE:

689290-74

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Best Local Similarity 49.8%;
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TELEX: 910/371-7166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
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 648
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STRANDEDNESS: Single
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REFERENCE/DOCKET NUMBER: PO
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TGACCGCTTC 657
                                                              GCTGACTATTCCCCGACTTCATCTTTGCCAACGTCAGTGAGGCAGATGACAGATATATCTG
                                                                                           GCCAAGGAAGCTGTTGGCTGAAAAGGTGGTCTATGTTGGCGTCTGGATCCCTGCCCTCCT
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                                 TCTCGACCTC 611
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/1/pna/US06_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US084_COMB.seq:*
/cgn2_6/ptodata/1/pna/US086_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US099B_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US090B_COMB.seq:*
/cgn2_6/ptodata/1/pna/US090B_COMB.seq:*
/cgn2_6/ptodata/1/pna/US090B_COMB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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| cgn2_6/ptodata/1/pna/US6001_COMB.seq:
| cgn2_6/ptodata/1/pna/US6003_COMB.seq:
| cgn2_6/ptodata/1/pna/US6005_COMB.seq:
| cgn2_6/ptodata/1/pna/US6006_COMB.seq:
| cgn2_6/ptodata/1/pna/US6006_COMB.seq:
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| cgn2_6/ptodata/1/pna/US6010_COMB.seq:
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| cgn2_6/ptodata/1/pna/US6011_COMB.seq:
| cgn2_6/ptodata/1/pna/US6013_COMB.seq:
| cgn2_6/ptodata/1/pna/US6015_COMB.seq:
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| cgn2_6/ptodata/1/pna/US6026_COMB.seq:
| cgn2_6/ptodata/1/pna/US6036_COMB.seq:
| cgn2
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Query Match

Length 멺

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; TYPE: DNA; ORGANISM: homo sapiens; FEATURE; I NAME/KEY: CDS; LOCATION: (54)..(1067)
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SEQ ID NO 1
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             TTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATCCATGAAG
                                                         CCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTACCCTTCCATATCTTGAGGGTCA
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Sequence 1, Application US/60269795
GENERAL INFORMATION:
APPLICANT: BYISTO! Myers Squibb Company
ITILE OF INVENTION: A NOVEL HUMAN G-PROTEIN COL
TITLE OF INVENTION: KIDNEY
FILE REFERENCE: D0077 PSP 1
CURRENT APPLICATION NUMBER: US/60/269,795
CURRENT FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 1081
TYPE: DNA
ORGANISM: homo sapiens
FEATURE:
NUMBER: COL
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LOCATION: (54)
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TCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGAGCTGCTTTT
                                                          ATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCT
                                                                                                      TGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAACTGGATCTTTGGAG
                                                                                                                     TGACCAGCCTCCCCTTCCCTGATTCACTACTACTATGCCAGTGGCGAAAACTGGATCTTTGGAG
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9336 C 9336

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; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-634-5
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APPLICANT: Edinger, Shlomit R
APPLICANT: Edinger, Shlomit R
APPLICANT: Gangolli, Esha A
APPLICANT: Malyankar, Uriel M
APPLICANT: Malyankar, Uriel M
APPLICANT: Millet, Isabelle
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-221
CURRENT APPLICATION NUMBER: US/10/023,634
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/256,025
PRIOR APPLICATION NUMBER: 60/255,163
PRIOR APPLICATION NUMBER: 60/255,163
PRIOR APPLICATION NUMBER: 60/272,929
PRIOR APPLICATION NUMBER: 60/274,864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/315,600 PRIOR FILING DATE: 2001-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/309,246
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RIOR FILING DATE: 2001-03-16
RIOR APPLICATION NUMBER: 60/277,880
RIOR FILING DATE: 2001-03-22
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APPLICANT: Colman, Steven D
APPLICANT: Spytek, Kimberly A
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Tchernev, Velizar T
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Zerhusen, Bryan D
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                                                                                                                                                                                                                                                            99.9%; Score 1079.4; DB 38; Length 1560;
99.9%; Pred. No. 5.9e-299;
tive 0; Mismatches 1; Indels 0; Gaps
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RESULT 6
US-09-475-790-2
; Sequence 2, Application US/09475790
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
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081 C 1081	0
320 GGAACCTTGAGCAAGCAAAGAAATTAGTTACTCAAACAACCCTTGAAATATTTCATTTA 137	13
021 GGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAACAACCCTTGAAATATTTCATTTA 108	. 10
60 TGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAAGTAAGCG 13	Db 12
CAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAAGTAAGCG 10	· •
00 CTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACCTGTTACTATATG 12	12
01 CTTACATCOTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACCTGTTACTATATG 96	•
1140 TTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATCCATGAAG 11	Db 11
841 TTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATCAGATCCATGAAG 900	9 VQ
1080 CCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTACCCTTCCATATCTTGAGGGTCA 1139	_
781 CCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTTACCCTTCCATATCTTGAGGGTCA 840	
020 ACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGCTAA 10	Db 10
21 ACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGCT	
0 CTGCAACTACT	
661 CTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTTGCTATACCACGATTATCC 720	
0 GTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTAATTTTGA 95	Db s
1 GTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTGATTTTGA 66	
40 TAGCTGTCATTCCGATGACCTTCTTGATCACATCAACCAGCAGGACCAACAGATCAGCCT 89	Db t
541 TAGCTGTCATTCCGATGACCTTCTTGATCACCATCAACCAAC	
780 CCATTCACAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGGATCATTTCACTGG 839	
481 CCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGGATCATTTCACTGG 540	
720 TCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATCACCCAATGAGCTGCTTTT 779	
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660 ATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCT 719	
361 ATTICATGIGIAAGTITATCCGCTTCAGCTTTCAGTTTTCAACCTATATACCAACCA	•
600 TGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAACTGGATCTTTGGAG 659	DЬ
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1 GACCTIGGAAGAGCAGCACCAICATIAIGCIGAACCIGGCCIGCACAGAICIGCIGIAIC 30	
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RESULT 8 US-09-785-276A-25756; Sequence 25756, Ap.

Application US/09785276A

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REPRICANT: Schlegel, Robert
APPLICANT: Endege, Wilson
APPLICANT: MORAHAN, John
ITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
ITILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PRI
ITILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PRI
ITILE OF INVENTION: HUMAN PROSTATE CANCER
FILL REFERENCE: MRI-007B
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/213,319
PRIOR APPLICATION NUMBER: 60/213,319
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-10-18
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NAME/KBY: misc feature

LOCATION: 1, 2, 3, 4, 5, 6, 7

OTHER INFORMATION: n = A,T,C
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Pred. No. 6.2e-299;
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; LOCATION: 1, 2, 3, 4, 5, 6, 7, 8
; OTHER INFORMATION: n = A,T,C or
US-09-785-276A-30042
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PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR PILING DATE: 2000-12-13
NUMBER: 60/255,281
PRIOR PILING DATE: 2000-12-13
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US-09-785-276A-30042
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Best Local Similarity
Matches 1080; Conserv
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 30042
LENGTH: 1729
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: LICENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT FILING DATE: 2001-02-16
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RESULT 11
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Sequence 40, Application US/60261974

GENERAL INFORMATION:

APPLICANT: Beasley, Ellen

TITLE OF INVENTION: ISOLATED HUMAN NUCLEAR HORMONE RECEPTOR

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN NUCLEAR

TITLE OF INVENTION: HORMONE RECEPTOR PROTEINS, AND USES THEREOF

TILE REFERENCE: CL001096-PROY

CURRENT APPLICATION NUMBER: US/60/261,974

CURRENT FILING DATE: 2001-01-17

NUMBER OF SEQ ID NOS: 237

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 40
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SEQUENCE 234, Application US/60205423
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
ITITLE OF INVENTION: ISOLATED HUMAN G-PROTEI
ITITLE OF INVENTION: RECEPTORS, NUCLEIC ACII
ITITLE OF INVENTION: PROTEINS, AND USES THER
FILE REFERENCE: CL000563
CURRENT APPLICATION NUMBER: US/60/205,423
CURRENT FILING DATE: 2000-05-19
UNMER OF SEQ ID NOS: 494
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 234
LENGTH: 8161
TYPE: DNA
ORGANISH: HUMAN
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Sequence 235, Application US/60205423
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN
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Search completed: January 30, 2003, 09:39:16 Job time : 3519 secs

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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Pending Patents NA New:*

1: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/US010_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/US010_NEW_COMB.seq:*
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1081
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Copyright (c) 1993 - 2003 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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10.00 9.3 9.0 8.9 8.7 8.7 8.7	100.0 100.0 93.8 93.8 93.7 93.7 93.7 12.4 12.4 12.4 12.1 12.1	Query
2025 2025 2025 984 1571 1428 1041 1041 1041 1041 2807	1414 19905 110114 110114 110114 110114 110114 110114 110111 110111 110111	Length
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US-09-814-915A-74 US-10-305-720-1482 US-09-461-436B-41 US-10-305-720-1108 US-09-461-436B-57 US-10-152-319A-2045 US-10-278-107-35 US-10-321-807-13 US-10-321-807-87 US-10-321-807-87 US-10-321-807-87	US-10-017-161-525 US-10-270-144-3 US-10-270-144-1 US-10-188-405-7 US-10-188-405-7 US-10-188-107-27 US-10-278-107-33 US-10-278-107-33 US-10-276-774-102 US-10-276-774-102 US-10-276-772-105 US-10-276-774-102 US-10-276-774-105 US-10-301-301-301-301-301-301-301-301-301-	ID
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83.8	83.8	84	84	84	84	84	84	84	87.2	87.6	87.6	87.6	87.6	90.4	90.8	90.8	90.8	0.0
7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.8	8.1	8.1	8.1	8.1	8.1	8.4	8.4	8.4	8.4	0.
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence			Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	sequence
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; NAME/KEY: CDS
; LOCATION: (201)..(1214)
US-10-017-161-525
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Best Local Similarity 100.0%;
Matches 1081; Conservative (
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APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
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CURRENT FILING DATE: 2002-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: source
LOCATION: (1)..(1414)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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241 GACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATC 300
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                                                                                                                                                                                                                                                                                                      148 CATATTGCCAAACTGAACTCTCTTGTTTTCTTGCAAGATGAAAGGAGACAACCATGAATG 207
                                                                                                                                                                                                                                               61 AGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCGATTATGCAGCTGCTTTTGGAA 120
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                                                                                    TCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTTTCAAAATGA 240
                                                                                                                                                                                                                  AGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCCGATTATGCAGCTGCTTTTGGAA
                                          AATGCAGTAGTGATATCCACTTACATTTTCAAAATGA 387
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Pred. No. 8.4e-295;
); Mismatches 0;
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US-10-270-144-1
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; LENGTH: 1014
; TYPE: DNA
ORGANISM: Human
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GENERAL INFORMATION:
APPLICANT: WEI, MING-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000750CON
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Best Local Similarity
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CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/205,196
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                     ATCCTCTTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGAGC
                                                                      GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTTTC 233
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CCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGGATCATT
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GENERAL INFORMATION:

APPLICANT: Tian, Hui
APPLICANT: Dai, Kang
APPLICANT: Chen, Jin-Long
APPLICANT: Chen, Jin-Long
APPLICANT: Chen, Jiagang
APPLICANT: Chen, Jiagang
APPLICANT: Thlarik Inc.
TITLE OF INVENTION: Novel Receptors
FILE REFERENCE: 018781-008410US
CURRENT APPLICATION UNMBER: US/10/188,405
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US 60/302,800
PRIOR TILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 1014
TYPE: DNA
OPERANTEM: 1014
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; OTHER INFORMATION: human TGR164
US-10-188-405-7
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Best Local Similarity
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                                                                                                                                                                                                            ORGANISM: Homo sapiens
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GTAAGCGGGAACCTTGAGCAAAGCAAAGAAATTAGTTACTCAAACAACCCTTGA 1014
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                                                                                                       93.8%; Score 1014; DB 6; I
100.0%; Pred. No. 5.9e-276;
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APPLICANT: REDDY, Roopa
APPLICANT: KALLICK, Deborah A.
APPLICANT: TANG, Y. Tom
APPLICANT: AU-YOUNG, Janice
ITILE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0096 USA
CURRENT APPLICATION NUMBER: US/10/278,141
CURRENT FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: 60/208,834
PRIOR FILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,566
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 60/207,628
PRIOR APPLICATION NUMBER: 60/205,628
PRIOR APPLICATION NUMBER: 60/208,628
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: 60/208,861
PRIOR APPLICATION NUMBER: 60/208,861
PRIOR APPLICATION NUMBER: 60/208,861
PRIOR APPLICATION NUMBER: 60/208,222
PRIOR APPLICATION NUMBER: 60/206,222
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PERL PROGram
LENGTH: 1014
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US-10-278-141-10
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APPLICANT:
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APPLICANT: LU, Dyung Aina M.
APPLICANT: THORNTON, Michael
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ELLIOTT, Vicki S.
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KHAN, Farrah A.
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; ORGANISM: Homo sapiens
; FEATURE;
; NAME/KEY: misc_feature
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US-10-278-141-10
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Pred. No. 1.7e-275;
0; Mismatches 1;
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APPLICANT: AU-YOUNG, Janice
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0096 PCT
CURRENT APPLICATION NUMBER: US/10/296,081
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 60/205,628; 60/207,566; 60/208,834; 60/208,861
PRIOR APPLICATION NUMBER: 60/205,628; 60/207,566; 60/208,834; 60/208,861
PRIOR APPLICATION NUMBER: 2000-05-22; 2000-05-25; 2000-06-02; 2000-06-02
SOFTWARE: PERI DATE: 2000-05-18; 2000-05-22; 2000-06-02; 2000-06-02
SOFTWARE: PERI PROGRAM
SOFTWARE: PERI PROGRAM
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 6575963CB1
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Best Local
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BLLIOTT, Vicki S.
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KHAN, Farrah A.
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Pred. No. 1.7e-275;
0; Mismatches 1;
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; TYPE: DNA
; ORGANISM: Homo sapiens
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(545)
; OTHER INFORMATION: n = a,t,c or g
US-10-276-774-102 RESULT 9
US-10-276-774-102/c
Sequence 102, Application US/10276774; GENERAL INFORMATION: PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: CUSTOM
SEQ ID NO 102
LENGTH: 545 APPLICANT: Hyseq, Inc.
APPLICANT: Tang, Y, Tom et al
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27

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265 TTATGCTGAACCTGG-CCTGCACAGATCTGCTG-TATCTGACCAGCCTCCCCTTCCTGAT 322

412 383 472 323

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353

413

Best Loca Matches

Local Similarity les 526; Conservat

Conservative

44.48; 98.78;

Score 479.8; DB 6; Pred. No. 2e-125; 0; Mismatches 2;

Length Indels

545; 5

Gaps

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Query Match

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RESULT 12
US-10-305-720-1456
US-10-305-720-1456
; Sequence 1456, Application US/10305720
; GENERAL INFORMATION:
APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OP INVENTION: Composition for the Detection of Signaling Pathway Gene Expressi
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                                                                CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL PROGRAM
SEQ ID NO 1456
LENGTH: 3055
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RESULT 13
US-10-272-983-35
; Sequence 35, Application
; GENERAL INFORMATION:
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; NAME/KEY: misc_feature
; OTHER IMFORMATION: GenBank ID No: g798835
US-10-305-720-1456
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Best Local Similarity
Matches 424; Conserv
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                                                                         CTAGACCATTAGCTGCTCTGAACACCTTTTGGTAACCTGTTACTATATGTGGTGGTCAGCG
                                                CAAGAGGTCTAGCAAGTCTCAACAGTTGTGTGGACCCCATTCTCTATTTCTTGGCCGGAG
                                                                                                                 ATTTTCAGACCCCAGCAATGTGTGCTTTCAATGACAGGGTTTATGCCACGTATCAGGTGA
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Pred. No. 1e-27;
0; Mismatches 408;
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US/10272983

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Sequence 20, Application US/10311671 GENERAL INFORMATION:
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                                    INVENTION: G-PROTEIN COUPLED RECEPTORS
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BAUGHN, Mariah R.
HAFALIA, April J. A.
NGUYEN, Danniel B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INCYTE GENOMICS, INC.
                                                                                                                                                                                                                                                                                                                                                                                          GANDHI, Ameena R. KALLICK, Deborah A. GRIFFIN, Jennifer A.
                                                                                                                                                                                                                                                                                                ARVIZU, Chandra S.
LU, Dyung Aina M.
TRIBOULEY, Catherine
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SOFTWARE: PERL Program

SEQ ID NO 20
LENGTH: 1542

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 3485895CB1
US-10-311-671-20
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CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/US01/19275
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,483
PRIOR PFLICATION NUMBER: 60/213,954
PRIOR PFLICATION NUMBER: 60/213,954
PRIOR PFLICATION NUMBER: 60/215,209
PRIOR APPLICATION NUMBER: 60/215,209
PRIOR APPLICATION NUMBER: 60/215,209
PRIOR APPLICATION NUMBER: 60/216,595
PRIOR FILING DATE: 2000-06-29
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/218,936
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
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Best Local Similarity 49.3%;
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                                                                                                        ААСАGATCAGCCTGTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTAC
                                                                                                                                            GTTTTAGTĀACCTTĀĠAGTTĀCTĀCCCĀTĀCTTCCCCTTĀTĀĀĀTCCTGTTĀTĀĀCTGĀC
                                AACCTGATTTTGACTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCTAT 707
                                                                      AATGGCACCACCTGTAATGATTTTGCAAGTTCTGGAGACCCCAACTACAACCTCATTTAC
AGCATGTGTCTAACACTGTTGGGGTTCCTTATTCCTCTTTTTGTGATGTGTTTTCTTTAT
                                                                                                                                                                                                                  TTCCGAGAACACCTTCTGCAAAAGAAAGAGTTTGCTATTTTAATCTCCTTGGCCATTTGG
                                                                                                                                                                                                                                                     AIGAGCIGCITITCCAITCACAAAACICGAIGTGCAGITGTAGCCIGIGCTGIGGIGTGG 527
                                                                                                                                                                                                                                                                                                                               AGCAGCATCCTCTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGATCATTCACCCA
                                                                                                                                                                                                                                                                                           ACCAGCATTCTCTCTCACTTTTATCAGCATAGATCGATACTTGATAATTAAGTATCCT 578
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Pred. No. 5.8e-27;
0; Mismatches 433
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RESULT 15 US-10-311-671-20

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

APPLICANT: APPLICANT: APPLICANT:

GRAUL, Richard YAO, Monique G.

CHAWLA, Narinder

APPLICANT:

APPLICANT

APPLICANT

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

Henry Farrah A.

APPLICANT: APPLICANT: APPLICANT:

APPLICANT:

RAMKUMAR, Jayalaxmi AU-YOUNG, Janice K. ELLIOTT, Vicki S.

APPLICANT:

APPLICANT: APPLICANT: APPLICANT

HERNANDEZ, ROBERTO WALSH, Roderick T. BOROWSKY, Mark L. THORNTON, Michael B.

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ch comple	936 ACC 1059 AGT	876 TCC 999 TGC	822 TTC 939 TAT	762 CAG 879 GAA	708 ACC
rch completed: January 30, 2003, 07:08:00	936 ACCTTTGGTAACCTGTTACTATATGTGGTGGTCAGCGACAACTT 979	876 TCCATTGAGAATCAGATGCATGAAGCTTACATGGTTTCTAGACCATTAGCTGCTCTGAAC 935	822 TTCCATATCTTGAGGGTCATTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGT 875	762 CAGAAAGCACGAAGGCTAACCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTTACCC 821	708 ACCACGATTATCCACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAG 761
	2	AGCTGCTCTGAAC	AGTTGT	ATGTTTTTACCC	CAGCTGCCTTAAG
		935 1058	875 998	821 938	761 878

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; ORGANISM: Homo
JS-10-272-983-35
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LENGTH: 1005
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Best Local Similarity
Matches 436; Conserv
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SOFTWARE: PatentIn Ver. 2.1
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CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US/99/417,044
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 60/109,213
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR APPLICATION NUMBER: 60/120,416
PRIOR FILING DATE: 1999-02-16
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PRIOR APPLICATION NUMBER: 60/136,567
PRIOR FILING DATE: 1999-05-28
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APPLICANT: Dang, Huong T.
APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
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FILING DATE: 1999-05-28
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  GTTTTAGTAACCTTAGAGTTACTACCCATACTTCCCCCTTATAAATCCTGTTATAACTGAC
                                          AGCAGCATCCTCCTCCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCA 467
                                                                                                                                                                                                                                                                                                                                                                    GACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATAAGGAGTTATGCCAATGG---AAAC 261
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                                                                                                                                                                                    ACCAGCATTCTCTCTCTCACTTTTATCAGCATAGATCGATACTTGATAATTAAGTATCCT 381
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                                                                                           TTCCGAGAACACCTTCTGCAAAAGAAAGAGTTTGCTATTTTAATCTCCTTGGCCATTTGG
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Pred. No. 5e-27;
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CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 1352
LENGTH: 1436
TYPE: DNA
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US-10-264-237-1352
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 436; Conservative
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA131P1
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                                                                                                                                                                                                                                                                                                                                      GCAACTTGCAAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAAAGTACTACCTTTCCATT 176
                                                                                                                                                                                                                                                                                                                                                                               GCTGCTTTTGGAAATTGCACTGATGAAAACATCCCACTCAAGATGCACTACCTCCCTGTT 167
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TGGATATATGGAGACGTGCTCTGCATAAGCAACCGATATGTGCTTCATGCCAACCTCTAT
                                      TGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTAT 407
                                                                                 GACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATAAGGAGTTATGCCAATGG---AAAC
                                                                                                                            GATCTGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAAAC 347
                                                                                                                                                                     ATTTTCAAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACA 287
                                                                                                                                                                                                                                                       TTTTATGGGATTGAGTTCGTTGTGGGAGTCCTTGGAAATACCATTGTTGTTTACGGCTAC
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Pred. No. 5.7e-27;
0; Mismatches 433;
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TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/10/270,857
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: US 09/908,593
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 08/781,456
PRIOR FILING DATE: 1997-01-10
PRIOR FILING DATE: 1997-01-10
PRIOR APPLICATION NUMBER: US 60/009,902
PRIOR APPLICATION NUMBER: US 60/009,902
PRIOR FILING DATE: 1996-01-11
NUMBER OF SEQ ID NOS: 9
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JS-10-270-857-1
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Best Local Similarity 49.9
Matches 438; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1
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                                               TGGATATATGGAGACGTGCTCTGCATAAGCAACCGATATGTGCCTATGCCAACCTCTAT
                                                                                     TGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTAT 407
                                                                                                                                  GACTTAGCTTTTCTGTGCACCCTCCCCATGCTGATAAGGAGTTATGCCAATGG---AAAC 352
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                                                                                                                                                                                                                                                                                                                                                                                               GCAACTTGCAAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAAAGTACTACCTTTCCATT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGCTTTTGGAAATTGCACTGATGAAAACATCCCACTCAAGATGCACTACCTCCCTGTT 167
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CURRENT APPLICATION NUMBER: US/10/270,587
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: US 09/908,593
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 08/781,456
PRIOR APPLICATION NUMBER: US 08/781,456
PRIOR PILLING DATE: 1997-01-10
PRIOR APPLICATION NUMBER: US 60/009,902
PRIOR PILING DATE: 1996-01-11
NUMBER OF SEQ ID NOS: 9
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                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
                                                                                                                                                      Matches
                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Human G-Protein Coupled Receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Li, Yi
                                                                                                                                                                                                                                               LENGTH: 1428
TYPE: DNA
ORGANISM: Homo sapiens
                                                                       116
168 ATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTAC
                                                                                             108 GCTGCTTTTGGAAATTGCACTGATGAAAACATCCCACTCAAGATGCACTACCTCCCTGTT 167
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                                                                 GCAACTTGCAAAAACTGGCTGGCAGCAGAGGCTGCCCTGGAAAAGTACTACCTTTCCATT 175
                                                                                                                                                      438;
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                                                                                                                                                                                                                                                                                                                                   version 3.1
                                                                                                                                                                      12.4%;
                                                                                                                                                  Score 134.4; DB 6;
Pred. No. 7.1e-28;
0; Mismatches 431;
                                                                                                                                                431;
                                                                                                                                                Indels
                                                                                                                                                                                     Length 1428;
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ORGANISM: HOMO SAPIENS
(S-10-278-107-33
                                                                           Query Match
Best Local Similarity
Matches 1013; Conserv
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                                                                                                                                                              SEQ ID NO 33
LENGTH: 1014
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 82
                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US/10/125,749
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: US/09/988,922
PRIOR FILING DATE: 2001-11-19
                                                                                                                                                                                                                                                           FILE REFERENCE: GP-70775B-C1
CURRENT APPLICATION NUMBER: US/10/278,107
CURRENT FILING DATE: 2002-10-21
                                                                                                                                                                                                                                                                                         APPLICANT: Eve mahe
TITLE OF INVENTION: HUMAN G PROTEIN-COUPLED RECEPTOR
TOTALE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
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APPLICANT: Yuan Zhu
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Joyce Yue Mao
Wendy S. Halsey
                                                                                                                                                                                                                                                                                                                                          Philippe Laurent Robert
Stephane Clement Krief
                                                                                                                                                                                                                                                                                                                                                                     Steven Ruben
George H. Poste
Michel Louis Souchet
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John W. Quillen, Jr.
Erin M. Toland
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Melanie Robbins
David Malcolm Duckworth
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Catherine E. Ellis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pankaj Agarwal
Randall Forrest Smith
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Nabil A. Elshourbagy
                                                                                                                                                                                                                                                                                                                                                                                                           Henry Sarau
                                                                                                                                                                                                                                                                                                                                                                                                                      Alexander Taylor
                                                                                                                                                                                                                                                                                                                                                                                                                                   Han Ngoc Trinh
                                                                                                                                                                                                                                                                                                                                                                                                                                              Steven Michael Foord
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               David Michalovich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usman
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Philip Graham Szekeres
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jeffrey Hill
                                                                              Conservative
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                                                                                        93.7%;
99.9%;
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                                                                         Score 1012.4; DB 6;
Pred. No. 1.7e-275;
0; Mismatches 1;
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Sequence 10, Application US/10296081
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: PATTERSON, Chandra
APPLICANT: LU, Dyung Aina M.
APPLICANT: LU, TYAN
APPLICANT: LU, YAN
                                                                                   RESULT 8
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GTAAGCGGGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAACAACCCTTGA
                                                    GTAAGCGGGAACCTTGAGCAAGCAAAGAAATTAGTTACTCAAACAACCCTTGA 1067
                                                                                                     CTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAA
                                                                                                                                                  CTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAA 1013
                                                                                                                                                                                                   CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTTGGTAACCTGTTA
                                                                                                                                                                                                                                   CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACCTGTTA 953
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Sequence 27, Application US/10321807
GENERAL INFORMATION:
APPLICANT: Chen, Rupong
APPLICANT: Dang, Huong T.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Lowitz, Kevin P.
TITLE OF INVENTION: Non-Endogenous, CC
TITLE OF INVENTION: Receptors
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-321-807-27
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CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: US/09/714,008
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: PCT/US99/23938
PRIOR APPLICATION NUMBER: PCT/US99/23938
PRIOR APPLICATION NUMBER: 60/166,088
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PRIOR APPLICATION NUMBER: 60/166,099
PRIOR APPLICATION NUMBER: 60/166,099
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Best Local Similarity
Matches 1014; Conserv
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NUMBER OF SEQ ID NOS: 133
SOFTWARE: PatentIn version 3.0
SEQ ID NO 27
LENGTH: 1014
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DR FILING DATE: 1999-12-23
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DR FILING DATE: 1999-12-23
DR APPLICATION NUMBER: 60/181,749
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APPLICATION NUMBER: 60/166,369
FILING DATE: 1999-11-17
TCAGCCTGTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTG
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Sequence 3, Application US/10270144
GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENC
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000750CON
CURRENT APPLICATION NUMBER: US/10/270,144
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/205,196
PRIOR FILING DATE: 2000-05-18
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SOFTWARE: FastSEQ for Windows Version
; SEQ ID NO 3
; LENGTH: 9905
; TYPE: DNA
; ORGANIEM: Human
US-10-270-144-3
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Best Local Similarity
Matches 1081; Conserv
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                      TTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATCCATGAAG 900
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; LENGTH: 8161
; TYPE: DNA
; ORGANISM: HUMAN
US-60-205-423-235
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CURRENT FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 494
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 235
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Best Local Similarity
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            ACCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTACCCTTTCCATATCTTGAGGGTC 839
                                                                                                                                                    CTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCTATACCACGATTATCC
                                                                                 ACACTCTGACCCATGGACTGCAAACTGACAGCTG-CCTTAAGCAGAAAGCACGAAGGCTA 779
                                                                                                                                 CTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCTATACCACGATTATCC
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Pred. No. 1.9e-
0; Mismatches
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Sequence 236, Application US/60205423
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
ITILE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
ITILE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENC.
ITILE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000563
CURRENT APPLICATION NUMBER: US/60/205,423
CURRENT FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 494
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 236
LENGTH: 8161
TYPE: DNA
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Best Local Similarity 99.8
Matches 1080; Conservative
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TCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGAGCTGCTTTT
                                             ATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCT
                                                                                                      TGACCAGCCTCCCCTTCCCTGATTCACTACTATGCCAGTGGCGAAAACTGGATCTTTTGGAG
                                                                                                                                                 GACCTTGGAAGAGCAGCATCATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATC
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                                                                                       TGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAAACTGGATCTTTGGAG
                                                                                                                                                                                                         TCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTTTCAAAATGA
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; LENGTH: 43262
; TYPE: DNA
; ORGANISM: Human
US-60-261-974-40
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Matches 1080; Conserv
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           CTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCTTTGGTAACCTGTTACTATATG
                                                        TTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATCAGTTGAAG
                                                                        TTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATCCATGAAG
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RESULT 12
US-60-205-423-233
; Sequence 233, Application US/60205423
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000563
; CURRENT FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 494
; SOFTWARE: FRASUSEQ FOR Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 8161
; TYPE: DNA
; ORGANISM: HUMAN
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Best Local Similarity 99.8%;
Matches 1080; Conservative
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                                                                                 TCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGAGCTGCTTTT
                                                                                                                                                         ATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCT
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                                                                                                    TCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGAGCTGCTTTT 480
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                          CCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGGGATCATTTCACTGG
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Sequence 29927, Application US/09785276A

GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Schlegel. Nobert
ITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
ITLE OF INVENTION: HUMAN PROSTATE CANCER
ITLE OF INVENTION: HUMBER: 60/2-16
PRIOR APPLICATION NUMBER: 60/2-16
PRIOR APPLICATION NUMBER: 60/207, 454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/2-19,007
PRIOR APPLICAT
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                                                                                                         SEQ ID NO 29927
LENGTH: 1729
TYPE: DNA
ORGANISM: Homo:
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                                              TTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATCCATGAAG
                                                                                CCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTACCCTTTCCATATCTTGAGGGTCA
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; LOCATION: (294)...(1307)
US-09-475-790-2
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SEQ ID NO 2
LENGTH: 1729
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Best Local Similarity
Matches 1080; Conserv
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TITLE OF INVENTION: Novel Seven-Transmembrane
TITLE OF INVENTION: Proteins/G-Protein Coupled Receptors
FILE REFERENCE: 5800-67
CURRENT APPLICATION NUMBER: US/09/475,790
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 34
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.9%; Score 1079.4; DB 1
99.9%; Pred. No. 6.2e-299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Sequence 24015, Application US/09785276A

GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Schlege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: MORADAN, John
ITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR ITILE OF INVENTION: HUMAN PROSTATE CANCER
FILLE OF INVENTION: HUMAN PROSTATE CANCER
FILLE REFERENCE: MRI-007B
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR APPLICATION NUMBER: 60/183,319
APRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/183,319
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                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens ; PEATURE: ; PEATURE: ; NAME/KEY: misc_feature ; LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, OTHER INFORMATION: n = A,T,C or G US-09-785-276A-24015
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SOPTWARE: FASTSEQ for Windows Version
SEQ ID NO 24015
LENGTH: 1729
TYPE: DNA
                                                                                                                                                                   Query Match 99.9%;
Best Local Similarity 99.9%;
Matches 1080; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/219,007 PRIOR FILING DATE: 2000-07-18
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                                                                                                                                                                                  Score 1079.4; DB 30; Pred. No. 6.2e-299;
                                                                                                                                                                   Mismatches
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Sequence 3, Application US/09634656

GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al
TITLE OF INVENTION: ISCLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000750
CURRENT APPLICATION NUMBER: US/09/634,656
CURRENT APPLICATION NUMBER: 00/205,196
PRIOR APPLICATION NUMBER: 60/205,196
PRIOR PILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 9905
TYPE: DNA
COGANISM: Human
S-09-634-656-3
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JS-09-634-656-3
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                                                   Query Match 100:0%; Score 1081; DB 24; Length 9905; Best Local Similarity 100.0%; Pred. No. 4.9e-299; Matches 1081; Conservative 0; Mismatches 0; Indels 0;
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1 CATATTGCCAAACTGAACTCTCTTGTTTTCTTGCAAGATGAAAGGAGACAACCATGAATG 60
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9335	76 GGAACCTTGAGCAA	뫄
1080	021 GGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAACAACCCTTGAAATATTTCA	Ş
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10	61 TGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAAGTAA	Ş
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900	841 TICGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATCCATGAAG	을 성
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840	781	Ś
90		당
780	721 ACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGG	\$
8975	8916 CTGCAACTATTCTGCCTCCCCTTGGTGATAGTGACACTTTTGCTATACCACGATTATCC	문
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660	01 GTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTGATTT	Ş
8855	96 TAGC	당
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87		망
υ 4	81 CCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGGATCATTT	Ś
87	8676 TCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGAGCTGCTTTT	당
480	21 TCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTCACCCAATGAGCTC	Ş
8675	16	망
420	61 ATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGCAI	Ş
360	301 TGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGGCGAAAACTGGATCTTTGGAG	유 성
8555	96 GACCTTGGAAG	
300	41 GACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGC	Ś
8495	36	В
240	81 TCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATC	8
180	21 ATTGCACTGAT	B 8
8375	16 AGCCACTAGACTATTTAGCA	망
120	1 AGCCACTAGACTATTTAGCAAAIGCTTCTGATTTCCCCGATTATGCAGCTGCTTTTC	8
8315		뮍

1081 C 1081

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; LENGTH: 1081
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)..(1064)
US-10-010-568-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 1, Application US/10010568
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPI
TITLE OF INVENTION: KIDNEY
FILE REFERENCE: D0077 NP
CURRENT APPLICATION NUMBER: US/10/010,568
CURRENT FILING DATE: 2001-12-07
FRIOR APPLICATION NUMBER: US 60/251,926
PRIOR APPLICATION NUMBER: US 60/259,795
PRIOR APPLICATION NUMBER: US 60/269,795
PRIOR APPLICATION NUMBER: US 60/269,795
PRIOR APPLICATION NUMBER: US 60/269,795
PRIOR FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 55
SOFTMARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: DNA
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Best Local Similarity
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US-60-311-340-1
US-09-914-408A-27
US-09-885-453-2
US-09-995-543-27
US-09-569-137-1
US-09-58-922-33
US-10-025-749-33
US-10-125-749-33
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Sequence 1, Application US/60251926
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: A NOVEL HUMAN G-PROTE;
TITLE OF INVENTION: KIDNEY
TITLE OF INVENTION: KIDNEY
FILE REFERENCE: D0077 PSP
CURRENT APPLICATION NUMBER: US/60/251,926
CURRENT FILING DATE: 2000-12-07
JG-NUMBERSOP SEQ ID NOS: 35
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PRIOR APPLICATION NUMBER: UK 0021484.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 24
SOPTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 2051
TYPE: DNA
ORGANISM: Homo sapiens
IS-09-944-807-20
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; ORGANISM: Homo sapiens
US-09-962-832-218
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JS-09-944-807-20

Sequence 20, Application US/09944807

Sequent No. US20020119494A1
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                                                                                                     Query Match 7.7%;
Best Local Similarity 52.0%;
Matches 186; Conservative
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Best Local Similarity 52.0%;
Matches 186; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Method for identifying substances which positively TITLE OF INVENTION: influence inflammatory conditions of chronic TITLE OF INVENTION: inflammatory airway diseases FILE REFERENCE: 082 00n CURRENT APPLICATION NUMBER: US/09/944,807 CURRENT FILLING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/962,832
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,077
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,280
PRIOR APPLICATION NUMBER: US/60/235,280
PRIOR FILING DATE: 2000-09-25
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                                      183 TTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTTACATTTTCAAAATGAGA 242
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TTTATCTTTGGGCTTCTGGGCAATGGCCCTTGCCCCTGTGGATTTTCTGTTTTCCACCTCAAG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCACGGTGGTGGCGGTAGACAGGTATTTCCGGGTGGTCCATCCCCACCACGCCCTGAAC 471
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                                                                                                Score 82.8; DB 10;
Pred. No. 2e-14;
0; Mismatches 172;
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JS-09-788-133-1
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                                      . LOCATION: (1)..(1020) 
JS-09-788-133-1
                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/788,133
CURRENT FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 1
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CURRENT PILING DATE: 2000-11-30

NUMBER OF SEQ ID NOS: 101

SOFTWARE: pt_FL_genes Version 2.0

SEQ ID NO 26

SEQ ID NO 26
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Best Local Similarity
Matches 207; Conserv
Query Match
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09788133 Patent No. US20020052001A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: CDS
LOCATION: (232)..(1272)
NAME/KEY: misc_feature
LOCATION: (1)...(1700)
OTHER INFORMATION: n = a,t,c o
                                                                                                                                                                                                                                                                                            FILE REFERENCE: P79011
                                                                                                                                                                                                                                                                                                               APPLICANT: GLAXO GROUP LTD TITLE OF INVENTION: ASSAY
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                                                                                FEATURE:
NAME/KEY: CDS
                                                                                                                      TYPE: DNA
ORGANISM: homo sapiens
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TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No. 1.1e-17;
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                                                                                              SOFTWARE: PatentIn Ver.
SEQ ID NO 2143
LENGTH: 1670
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Patent No. US20020142981A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
                                                                                                                                                                                                                                                                                                                           APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Horne, Darci T. APPLICANT: Vockley, Joseph APPLICANT: Scherf, Uwe
                     ORGANISM: Homo sapiens FEATURE:
                                                                   TYPE: DNA
OTHER INFORMATION: Genbank Accession No. US20020142981A1 L06797
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; TYPE: DNA; ORGANISM: Homo sapiens JS-09-828-478-1
                                                                                                                         FILE REFERENCE: 04974.00458
CURRENT APPLICATION NUMBER: US/09/828,478
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 60/195,196
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/254,876
PRIOR FILING DATE: 2000-12-13
NUMBER: OF SEQ ID NOS: 16
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; ORGANISM: Homo sapiens
US-09-826-791-1
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CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 0008504.3
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/198,367
PRIOR FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Xiao, Yonghong
TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
TITLE OF INVENTION: Protein
                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09828478 Patent No. US20020155528A1
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Best Local Similarity
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TITLE OF INVENTION: No. US20010039037A1el Polypeptide
FILE REFERENCE: PC10914ADAM
                                                                    LENGTH: 1041
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Pred. No. 8.5e-18;
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GENERAL INFORMATION:

APPLICANT: Pfizer Inc

FITTLE OF INVENTION: No. US20010039037A1el Polypeptide

FILB REFERENCE: PC10914ADAM

CURRENT APPLICATION NUMBER: US/09/826,791

CURRENT FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 0008504.3

PRIOR FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: 60/198,367

PRIOR FILING DATE: 2000-04-19

NUMBER OF SEQ ID NOS: 6

NUMBER OF SEQ ID NOS: 6
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US-09-826-791-5
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Matches 207; Conserv
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Best Local
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Patent No. US20010039037A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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TCATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCCTTCAGGGCTG 286
                       TTATGCTGAACCTGGCCTGCACAGATCTGCTGTATCTGACCAGCCTCCCCCTTTCCTGATTC 324
                                                                     ATGGGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTT
                                                                                                        ATGCAGTAGTGATATCCACTTACATTTTCAAAATGAGACCTTGGAAGAGCAGCACCATCA 264
                                                                                                                                          TCAAGAGAGAATTTTTCCCCAATTGTATATCTGATAATATTTTTCTGGGGAGTCTTGGGAA 166
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                                                                                                                                                                                                                  Score 93.6; DB 10;
Pred. No. 8.7e-18;
0; Mismatches 189;
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Pred. No. 8.7e-18;
0; Mismatches 189;
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APPLICANT: Glaxo Group Limited
TITLE OF INVENTION: Polypeptide
FILE REFERENCE: QG1021
CURRENT APPLICATION NUMBER: US/09/943,798
CURRENT FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
SEQ ID NO 1
TYPE: DNA
ORGANISM: Homo mapiens
(S-09-943-798-1
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                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09943798
Patent No. US20020065215A1
GENERAL INFORMATION:
                                                               Query Match
Best Local Similarity
                                                Matches 831;
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                                                Conservative
                                            76.9%; Score 831; DB 10; I
100.0%; Pred. No. 1.6e-236;
tive 0; Mismatches 0;
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APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhao, Qing A.
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20020128187A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 787CIP2F
                                                                                                                                                                                                                                           RESULT 3
US-09-728-422-1
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                                                                                                                                                             Sequence 1, Application US/09728422
Patent No. US20020128187A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
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JS-08-472-840-60
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Patent No. 5763575
.GENERAL INFORMATION:
APPLICANT: SUNDELIN, JOHAN
APPLICANT: SUNDELIN, JOHAN
APPLICANT: SUNDELIN, JOHAN
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR NUMBER OF SEQUENCES: 63
                                                                                                                               Query-Match 9.0%; Score 97.8; DB 1; Length 2 Best Local Similarity 52.6%; Pred. No. 6e-20; Matches 213; Conservative 0; Mismatches 192; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 60:
                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/08/390,301
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ADDRESSEE: MORRISON & FOERSTER
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                                             295 CTGACCACGGTCTTTCTTCCGGTCGTCTACATTATTGTGTTTTGTGATTGGTTTTGCCCAGT 354
                                                                                    144 CTCAAGATGCACTACCTCCCTGTTATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGC 203
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                                                504 GTTGTAGCCTGTGCTGTGGTGGATCATTTCACTGGTAGCTGTC 548
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GGCGTCTCCTTGGCAATCTGGCTCCTGATTTTTCTGGTCACCATC
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Search completed: January 30, 2003, 06:48:46
Job time: 78 secs

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Best Local Similarity 52.0
Matches 213; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: SUNDEL
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APPLICATION NUMBER: US 08/390,301
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REGISTRATION NUMBER: 30,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                           562 TACATGGCCAACCTGGCCTTGGCCGACCTCCTCTGTCATCTGGTTCCCCCCTGAAGATC
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                  384 TTCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCTTCCTCACCTGTTTCAGCATCTTC 443
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/476,976
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                                                                           TCCTACCACCTACATGGCAACAACTGGGTCTACGGGGAGGCCCTGTGCAAGGTGCTCATT 681
                                                                                                                  CACTACTATECCAGTEGCEAAAACTEGATCTTTEGAGATTTCATETTAAGTTTATCCEC 383
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VENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
VENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
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Pred. No. 4.3e-20;
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US-08-474-410-1
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Best Local Similarity
Matches 213; Conserv
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FEATURE:
NAME/KEY:
LOCATION:
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APPLICATION NUMBER: US
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APPLICATION NUMBER: US 0
FILING DATE: 25-JAN-1995
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR
                                 502 AATGGCATGGCCCTCTGGATCTTCCCTTTTCCGAACGAAGAAGAAACACCCCGCCGTGATT
                                                              204 AATGCAGTAGTGATATCCACTTACATTTTCAAAATGAGACCTTGGAAGAGCAGCACCATC
                                                                                                 442 CTGACCACGGTCTTTCCTGCGTCGTCTACATTATTGTGTTTTGTGATTGGTTTTGCCCCAGT 501
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264 ATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATCTGACCAGCCTCCCCTTCCTGATT 323
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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No. 6043212
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Pred. No. 4.3e-20;
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; Patent No. 5629174
; GENERAL INFORMATION:
APPLICANT: SUNDELLI
APPLICANT: SCARBORG
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Best Local Similarity 57.5%;
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                                                                                                                                                                               ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0,
                                                                         ATTORNEY/AGENT INFORMATION: NAME: MURASHIGE, KATE H.
                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR AND
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 221
FELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283
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                                                                                                           APPLICATION NUMBER: FILING DATE: 26-JUJ CLASSIFICATION: 43:
                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                    STREET:
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LOCATION: 28..1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATGCCAGTGGCGAAAACTGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGC 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGAACCTGGCACTGGCGGACCTGATGTATGCCTGTTCACTACCCCTACTTATCTATAAC 282
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                                                                                                                                                                                                                                                                                                               Washington, D.C.
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                                                                                                                 26-JUL-1993
N: 435
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                                     22803-20006.00
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Pred. No. 7.3e-21;
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                                                                                                                                                                                                                                                                                                                                N.W.,
                                                                                                                                                                                     Version
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US-08-097-938-1
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08476000 Patent No. 5716789
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Best Local Similarity
Matches 213; Conserv
                   ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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NAME/KEY:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 CTCAAGATGCACTACCTCCCTGTTATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGC 203
     APPLICATION NUMBER:
                                                                                                                                                        COUNTRY:
                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1475 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                         Washington
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С
                                                                                                                                                                                                            2000 Pennsylvania Ave. N.W.,
                                                                                                                                                                                                                                           ARTION:
ARTION:
ANDELIN, JOHAN
SCARBOROUGH, ROBERT M.
SCARBOROUGH, ROBERT M.
AVENITION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
AVENTION: RECOMBINANT C140 RECEPTOR ENCODING THE RECEPTOR
                                                                                                                                                          USA
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                                                                                                                                                                                                                                  MORRISON & FOERSTER
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232
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52.6%;
US/08/476,000
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Pred. No. 4.3e-20;
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                                       Version #1.30
                                                                                                                                                                                                              Ste. 5500
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RESULT 5
US-08-446-088A-1
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                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,088A
FILING DATE: 19-MX-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Venneth n cibic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08446088A Patent No. 5691156
TELERAX: 919-881-3175
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1842 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                  NAME: Kenneth D. Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-71C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lustig, Kevin D.
TITLE OF INVENTION: DNA Encoding the Human P2U Receptor
TITLE OF INVENTION: Null Cells Expressing P2U Receptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTCACCCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCT 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGTGTGGGTTGGTGCTGGCCTGCCAGGCCCCGTGCTCTACTTTGTCACCACCAGC
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No. 5691156th Carolina
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Harden, Thomas K.
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Sullivan, Daniel M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weisman, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boucher, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laura
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ice Drawer 34009
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US-08-513-974B-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 41, Application US/08513974B Patent No. 6114139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.5%;
Best Local Similarity 52.9%;
Matches 222; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
                                                                                                                                                                                                                                                                             APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED
TITLE OF INVENTION: PRODUCTION, AND US
                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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FILING DATE: 1
CLASSIFICATION:
                           APPLICATION NUMBER:
                                                                                                                                                   COUNTRY: U
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STRANDEDNESS: sing
TOPOLOGY: linear
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                                                                                                                                                                                                Boston
                                                                                                                                                                                  3
                                                                                                                                                                                                                 130 Water Street
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                                                                                                                                                                                                                                                                                                                                Fujii, Ryo
Ohtaki, Tetsuya
Fukusumi, Shoji
                                                                                                                                                                                                                                                                                                                                                                                    Hosoya,
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Pred. No. 1.1e-21;
0; Mismatches 198;
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USE THEREOF
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JS-08-749-707-1
                                                                                                                                                                                                                                                                          Sequence 1, Application US/08749707
Patent No. 6063582
GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC NUMBER OF SEQUENCES: 14
ZIP: 20036-5869

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
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                                                                                                                                                                                         CITY: Washington
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                                                                                                                                                                                                                                       ADDRESSEE:
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1800 M Street, N.W.
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FEATURE:
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 1306
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-700
TELEPHX: 202-467-7176
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NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 15-NOV-CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 50.1
mes 380; Conservative
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GAAAAGCCTCTCAACTTGGTCATCATGGCAGTGGTAATCTTCTCTGTGCTTTTTACACCC
                                   CAGAAAGCACGAAGGCTAACCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTACCC 821
                                                                        TACAAGATTGCTCTCTTCCTAAAGCAGAGGAATAGGCAGGTTGCTACTGCTCTGCCCCCTT 1305
                                                                                                                                                     AGCATGTGTCTAACACTGTTGGGGGTTCCTTATTCCTCTTTTTGTGATGTGTTTCTTTTAT
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                                                                                                                  ACCACGATT----ATCCACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCAGCATTCTCTCTCACTTTTATCAGCATAGATCGATACTTGATAATTAAGTATCCT 1005
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Pred. No. 1.4e-29;
0; Mismatches 370;
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                                          GCATCCTCTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCA 459
                                                                                                               CCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTCACACCAACCTCTACACCA 371
                                                                                                                                                                     TCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCA 411
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                                                                                                                                                                                                                                                                               TGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAAACTGGA 351
                                                                                                                                                                                                                                                                                                                                     TCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAACCTTTCCATCTCTGACT
                                                                                                                                                                                                                                                                                                                                                                                        TCAAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATC 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTT 231
                                                                                                                                                                                                                           TTGCTTTCCTGTGCACCCTTCCCATCCTGATAAAGAGTTATGCCAAT---GATAAGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Site_1: XhoI; Site_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'db_xref="taxon:10090"
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57.5%;
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Pred. No. 1.2e-17;
0; Mismatches 145;
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                                                                                                                                                                                                                            308
                                                                                                                                                                                                                                                                                                                                                                                                                                               155 CTACCTCCCTGTTATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGT 214
455 GATCATTCACCCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCAGTTGTAGCCTG
                                             428
                                                                                                                                                                          335 CAGTGGCGAAAACTGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCA 394
                                                                                                                                                                                                                                                                275 CCTGGCCTGCACAGATCTGCTGTATCTGACCAGCCTCCCCTTCCTGATTCACTACTATGC 334
                                                                                                                                                                                                                                                                                                              248 CCTCTGGATCTTCCCGAACGAAGAAGAACACCCCGCCGTGATTTACATGGCCAA
                                                                                                                                                                                                                                                                                                                                         215 GATATCCACTTACATTTTCAAAATGAGACCTTGGAAGAGCAGCAGCATCATTATGCTGAA 274
                                                                                                                                                                                                                                                                                                                                                                                                    188 CTTTCTTCCGGTCGTCTACATTATTGTGTTTGTGATTGGTTTGCCCCAGTAATGGCATGGC 247
                                           TGGCAACATGTATTGCTCCATCCTCTTCATGACCTGCCTCAGCGTGCAGAGGTACTGGGT
                                                                                        TTTCAACCTGTATAGCAGCATCCTCTTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGT 454
                                                                                                                                 ACATGGCAACAACTGGGTCTATGGGGAGGCCCTGTGCAAGGTGCTCATTGGCTTTTTCTA
                                                                                                                                                                                                                          CCTGGCCTTGGCTGACCTCCTCTGTCATCTGGTTCCCCCTGGCCATTGCCTACCACCT 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M.A.G.E. Cons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence start: 25 High quality sequence stop: 799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 801)
NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nouse mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Site 2: NotI; Cloned unidirectionally. Primer: Ōlic Library constructed by Life Technologies. Investigat providing samples: Jeffrey Green, M.D., NIH" 228 c 193 g 213 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dev_stage="5 months"
lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 99.6; DB 13; Length 801; Pred. No. 2e-17; O; Mismatches 184; Indels O
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WAGE:4952433 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 233; Conserv
                           TGGTGTGGATCATTTCACTGGTAGCTGTCATTCCGATGACCTTCTTGATCACATCAACCA 579
                                                                                                        TTCACCCAATGAGCTGCTTTTCCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTG 519
                                                                                                                                                                                                                                                                                                                 CCTGCACAGATCTGCTGTATCTGACCAGCCTCCCCTTGCTGATTCACTATGCCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                              TGCCCGTGTCCTATGGCGTGGTGTGCGTGCTCGGGTTGTGCCTGAACGTCGTGGCTCTCT 649
TIGIGIGGGIGCIGGIGCIGGCCAGGCACCCGIGCICIACTICGICACCACCAGCG 1009
                                                                         TGCGCCCTCTGCACTCCCTGCGTTGGGGCCCGGGTTATGCCCGCCGGGTGGCTGCGG
                                                                                                                                                                               ACCTGTATAGCAGCATCCTCTCCTCACCTGTTTCAGCATCTTCCGCTACTGTGATCA 459
                                                                                                                                                                                                                  GTGACCACTGGCCATTTAGCACGGTGCTCTGCAAGCTGGTGCGTTTCCTCTTCTACACCA
                                                                                                                                                                                                                                                    GCGAAAACTGGATCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCA 399
                                                                                                                                                                                                                                                                                                                                                             ATATCTTCCTATGCCGCCTCAAAACCTGGAACGCCTCCACCACCTACATGTTTCACCTGG
                                                                                                                                                                                                                                                                                     CAGTTTCGGACTCTCTACGCAGCGTCCCTGCCGCTGTTGGTTTATTACTACGCCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end: BamHI. Host: DH10B.
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484. .1605
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/note="data_source:MGD, source key:MGI:105107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="6 days neonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
/db_xref="FANTOM_DB:5430432J15"
/db_xref="MGD:MGT:1897121"
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AK005013
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                                                                                                                                                                                           RS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Airakawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barshi, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hojmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchiomni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Sho, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., and uavanchi zaici v. Oshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and uavanchi zaici v.
5 (bases 1 to 3001)
Adachi, J., Aizawa, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone:1300015C04:purinergic receptor P2Y, G-protein coupled 2, full insert sequence.

AK005013
                                                                                                                                                                                  Wynshaw-Boris, A., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                 Nature 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                         Gallus gallus
Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                     Contact: Frazer Murray
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163 c 125 g 108 t
                                                        /note="Vector: pSPORT1; Site 1: Not1; Site 2: Sal1; Cloned
unidirectionally. Primer: Oligo dT. 5' adaptor sequence:
5' TCGACCTCGAG 3'; 3' adaptor sequence: 5'
                            clone_lib="BP_Chicken
                                                                                                                                                                   clone="ROS071808"
                                                                                                                                                                                     db_xref="taxon:9031"
                                                                                                                                                                                                 organism="Gallus gallus"
                                                                                                      dev_stage="Unknown"
lab_host="DH10B"
                                                                                                                                    tissue_type="Brain"
                                                                                                                                                                                                                                ocation/Qualifiers
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Neognathae; Galliformes; Phasianidae;
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Pred. No. 2.1e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T. Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., F.,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., R.,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                MGI:986966
                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Other_ESTs: uk27c10.x1
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Similarity 59.1%;
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Mammalia; Eutheria;
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                 /note="Organ: kidney; Vector: pME188-FL3; Site_1: DraIII (CACCATGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                                                                                                      /lab_host="DH10B"
                                                                                                                          /dev_stage="adult"
                                                                                                                                                                  clone_lib="Sugano mouse
                                                                                                                                                                                            /clone="IMAGE:1970226"
                                                                                                                                                                                                             /strain="C57BL"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                 location/Qualifiers
                                                                                                                                                  sex="female"
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s musculus cDNA (
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168 ATTTATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTAC
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                                                                GCAACTTGCAAAAACTGGCTGGCAGCAGCAGGCTGCCCTGGAAAAGTACTACCTTTCCATT 184
                                                                                                            GCTGCTTTTGGAAATTGCACTGATGAAAACATCCCACTCAAGATGCACTACCTCCCTGTT 167
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                                                                                                                                                                    210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, In
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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602466748F1 NIH_MGC_75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
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Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                            198
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                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                      /clone_lib="IMAGE_1594810"
/clone_lib="NAGE_1594810"
/clone_lib="NAGE_1594810"
/lab_host="DH10B_(T] phage-resistant)"
/lab_host="DH10B_(T] phage-resistant)"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC_3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACATGGGCG3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACATGGGCGGACATG_10)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
Contact: Larry A. Cogburn
University of Delaware
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Townsend Hall, Newark, DE 19717,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cogburn,L.A., Morgan,R. and Burnside,J.
ESTs from Normalized Chicken fat cDNA library-USDA/IFAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 302-831-1335
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Phasianinae; Gallus.
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       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      cogburn@udel.edu, www
Location/Qualifiers
                                                                                         /notee"Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each developmental agg (across strains); Single pass sequencing from 5'-end" 223 c 210 g 121 t 7 others
                                                                                                                                                                                               /dev_stage="Embryonic (d18,d19); post-hatch (d1,w3,w7,w9
                                                                                                                                                                                                                                                                       /clone="pgf2n.pk002.o6"
/clone_lib="Normalized Chicken
                                                                                                                                                                   /lab_host="E. coli EMDH10B"
                                                                                                                                                                                                                       tissue_type="Abdominal
                                                                                                                                                                                                                                                                                                                                                  organism="Gallus gallus"
|strain="Commercial broil
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   ٥,
                    Pred. No. 4.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257;
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                        mRNA sequence.
BQ038875
BQ038875.2 GI:20383637
                                                                                                                                                                                                                          mRNA
                                                                                                                                                                                                                                  BQ038875
B9911C.pk010.113 normalized chicken lymphoid cDNA library Gallus
gallus cDNA clone pgn1c.pk010.113 5' similar to
sp|p34996|p2YR CHICK P2Y PURINOCEPTOR 1 (ATP RECEPTOR) (P2Y1)
(PURINERGIC RECEPTOR) pir|S33733 G protein-coupled receptor -
chicken emb|CAA51716.1| (X73268) ATP receptor P2Y1 [Gallus gallus],
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Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Seq primer: M13 Reverse.
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//dev stage="fetal"
//dev stage="fetal"
//dev stage="fetal"
//lab_host="DHIOB (Life Technologies) (TI phage resistant)"
//note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-BOI is a normalized cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lemnon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA, synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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'clone_lib="UI-E-EO1"
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Pred. No. 8.4e-63;
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                                                                                                                                                                                                                                                                                                                      GGTACACGGGCGTCGTGCACCCGCTGAAGTCGCTGGGGAGGCTGAAGAAGAAGAACGCCG
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                      BQ396255 641 bp MISC ng19907.y1 NICHD XGC Emb6 s IMAGE:5383884 5', mRNA sequence
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Fax: 302-831-3411
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On Mar 27, 2002 tl
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University of Delaware
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Gallus gallus"
/db xref="taxon:9031"
/clone="pgn1c,pk010,113"
/clone_lib="normalized chicken lymphoid cDNA library"
/sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="thymus, bursa,
/lab_host="E.coli EMDH10B"
/note="Vector: pCMVSPORT 6"
199 c 172 g 128 t
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GI:21083932
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Pred. No. 3e-25;
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search completed: January 30, 2003, 06:47:52
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RESULT 14
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                  Human;
                                                    Human AXOR89 (G-protein coupled receptor) cDNA.
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                                                                                                                                                                                                                                                                          GTAAGCGGGAACCTTGAGCAAAGCAAAGAAAATTAGTTACTCAAACAACCCTTGA 1067
                                                                                                                                                                                                                                                                                                                                                      CTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAA 1013
                                                                                                                                                                                                                                                                                                                                                                                               CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTGTAACACCTTTTGGTAACCTGTTA 953
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 AXOR89 polypeptide;
ion; cancer; pain; a
                                                                                       (first entry)
e; G-protein coupled receptor; vaccine;asthma; Parkinson's Disease; diabetes;
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anorexia; bulimia; acute heart failure; hypotension; hypertension; ulcer; stroke; urinary retention; osteoporosis; angina pectoris; schizophrenia; myocardial infarction; allergy; benign prostatic hypertrophy; migraine; vomitting, psychotic; neurological disorder; anxiety; manic depression; delirium; Huntington's Disease; Gilles dela Tourette's syndrome; dementia; dyskinesia; gene; ss.
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Homo sapiens

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CDS
                   1..1014
/product= "Human AXOR89 protein"
          /*tag=
                             ocation/Qualifiers
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GB2365012-A.

13-FEB-2002

10-MAY-2001; 2001GB-0011437

11-MAY-2000; 2000US-0569137.

(SMIK) SMITHKLINE BEECHAM CORP SMITHKLINE BEECHAM PLC.

Elshourbagy N, Shabon ď

P-PSDB; 2002-332558/37. DB; AAE21803.

Novel AXOR89 polypeptide and polynucleotide encoding it, useful for identifying agonists and antagonists in the treatment of diseases associated with an AXOR89 imbalance, such as cancers, diabetes or

Claim 2; Page 37pp; English

The invention relates to an isolated AXOR89 polypeptide (G-protein CC coupled receptor) and its polynucleotide. The novel AXOR89 polypeptide CC and polynucleotide encoding the polypeptide, is useful for identifying CC and polynucleotide (Grandpolynucleotide) is useful for identifying CC agonists and antagonists (Grandpolynucleotide) that are potentially useful in treating conditions associated with an AXOR89 imbalance, such as CC bacterial, fungal or protozoan infections, cancers, pain, asthma, cCC parkinson's Disease, diabetes, obesity, anorexia, bulinia, acute heart CC failure, hypotension, hypertension, urinary retention, osteoporosis, CC angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign CC prostatic hypertrophy, migraine, vonitting, psychotic and neurological CC disorders, anxiety, schizophrenia, manic depression, delirium, dementia, CC dyskinesias, such as Huntington's Disease or Gilles dela Tourette's cyndrome. The polynucleotide sequence may also be used for chromosome CC localisation or tissue expression studies. The AXOR89 is used as a CC vaccine or to produce fusion proteins. The present sequence is human axond control of the produce fusion proteins. AXOR89 cDNA.

Sequence 1014 BP; 259 A; 263 C; 188 G; 304 T; 0 other;

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Best Local Similarity
                                                                                                                 Matches 1013;
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121
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          GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTTTC
                                                 ATGAATGAGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCGATTATGCAGCTGCT
                                                                                       ATGAATGAGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCCCCGATTATGCAGCTGCT
                                      Conservative
                                                                                                                        93.7%;
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                                                                                                              Score 1012.4; DB 2.
Pred. No. 8.5e-287;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    severe mental retardation, Huntington's disease and Tourette's syndrome. The present sequence encodes the P2Y1-like GPCR of the invention.
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                                                                     CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTGTGAACACCTTTGGTAACCTGTTA 953
                                                                                                             AGGGTCATTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATC
                                                                                                                          AGGGTCATTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATC
                                                                                                                                                                   AGGCTAACCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTACCCTTCCATATCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1014 BP; 258 A; 263 C; 189 G; 304 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.8%; Score 1014; DB 24; 100.0%; Pred. No. 2.9e-287;
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The present specifically claimed human cDNA sequence (located on CC chromosome 13) encodes a purinergic-related G-protein coupled receptor CC (GPCR) of the invention. GPCRs constitute a major class of proteins CC responsible for signal transduction within a cell. Upon binding of a CC ligand to the extracellular portion of a GPCR, a signal is transduced CC GPCR proteins can be divided into five families, family I contains the CC purinergic GPCRs (e.g. the P2Y receptors). P2Y receptors are CC analogues, some also respond to UTP. The invention comprises a human CC g-protein coupled receptor protein and encoding nucleic acids. The GPCR CC protein and nucleic acids of the invention are useful in the treatment of a disease or condition mediated by a human protease. The GPCR protein in biological fluids; identifying compounds which modulate of the protein in biological fluids; identifying compounds which modulate the activity of the GPCR, or the interaction of the GPCR and a molecule with which it normally interacts; and treating a disorder characterised by an absence of, or inappropriate expression of the GPCR protein. The GPCR mucleic acids of the invention are useful in diagnostic assays to identify changes in the GPCR mucleic acid that lead to pathology; CC controlling GPCR expression, and in gene therapy to treat patients with aberrant GPCR gene expression. The GPCR nucleic acids can also be used in the production of transgenic animals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated G-protein coupled receptor peptide useful for treating disorder characterised by absence of, in appropriate or unwanted expression of the receptor protein, and as immunogens to raise antibodies.
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P-PSDB; AA014027.
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08-AUG-2000; 2000US-0634656.
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Query Match
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                   CATGAAGCTTACATCGTTTCTAGACCATTAGCTGCTCTGAACACCCTTTGGTAACCTGTTA
                                                                                          AGGGTCATTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATC
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Pred. No. 2.9e-287;
0; Mismatches 0;
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The invention relates to an isolated P2Y-like receptor polypeptide CC (ABBB3818-ABB83819) which is also referred to in the specification as CC (ABBB3818-ABB83819) which is also referred to in the specification as CC (ABBB3818-ABB83819) which modulates P2Y receptor activity is useful to treat a cc subject having a disorder that is responsive to P2Y-like receptor CC modulation. The disorder is a disease of immunity or inflammation. The cc substance may also be used to manufacture a medicine for the treatment or CC prophylaxis of a disorder that is responsive to stimulation or modulation of P2Y-like receptor activity. Disorders which may be treated include CC colon cancers, asthma, COPD, Crohn's disease, irritable bowel syndrome, CC gastroenteritis and colitis, inflammatory bacterial infections, CC autoimmune diseases, dermatitis, yiral diseases, bacterial infections, CC autoimmune diseases, dermatitis, glomerulonephritis allergies, allergic crhinitis, inflammatory bain and general inflammation such as tendonitis, CC polymyositis or prostatitis. The invention provides alternative substances for the treatment of immunological and inflammatory diseases. The present sequence is that the P2Y-like receptor variant encoding gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An isolated P2Y-like receptor polypeptide (HIPHUM 0000037) which can used for the identification of agonists and antagonists which may be used to treat an immune or inflammatory disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-SEP-2000; 2000GB-0021524
06-SEP-2000; 2000GB-0021894
25-SEP-2000; 2000GB-0023444
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DB; ABB83819.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Page 28-29; 35pp; English.
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CC (a) assessing whether a patient is afflicted with prostate cancer; CC (b) monitoring the progression of prostate cancer in a patient; CC (c) assessing the efficacy of a test compound to inhibit prostate CC cancer in a patient; CC (d) assessing the efficacy of a therapy for inhibiting prostate cCC (d) assessing the efficacy of a therapy for inhibiting prostate cancer CC in a patient; CC (e) selecting a composition for inhibiting prostate cancer CC (f) assessing the prostate cell carcinoment.

CC (f) assessing the prostate cell carcinoment.
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Best Local Similarity 99.9
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781. CCATTCTGCTACTCCTTGCATTTTACGTATGTTTTTTACCCTTCCATATCTTGAGGGTCA 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is also useful as a pharmacodyanamic or pharmacogenomic marker.
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                                                                      ACACTCTGACCCATGGACTGCAAACTGACAGCTGCCTTAAGCAGAAAGCACGAAGGCTAA 780
                                                                                                                                          CTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCTATACCACGATTATCC
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etc., are used for diagnosis and (gene) therapy of diseases that are (in)directly associated with (I) or its expression products. No diseases are specified but as (I) is expressed only in thyroid tissue, (I) is presumed to be involved in regulation of thyroid function. The present

The invention relates to the human P2Y11i gene (I), including its 5' and 3' untranslated regions, located on chromosome 13 and encoding a G protein-coupled receptor. (I) and related mRNA, cDNA, protein, antibodies

Claim 5; Page 3; 5pp; German.

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                                                                                                New human P2Y1li gene, useful for treatment and diagnosis of associated diseases, and related proteins, antibodies and modulators, encodes G protein-coupled receptor
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                                                                                                                                                                                                                                                                                                                                                                           chromosome 13; G protein-coupled; receptor;
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Best Local Similarity
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(e) selecting
(f) assessing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastazed in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is also useful as a pharmacodyanamic or pharmacogenomic marker.
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              ATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCAGCATCCTCT
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                                                          CCATTCACAAAACTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGGATCATTTCACTGG
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Pred. No. 2.3e-306;
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Novel isolated nucleic acid molecule associated with cancerous state of

PTXRRXPXRX

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CC 26904, 38911 and 39404 protein-associated disorder characterised by
CC aberrant expression or activity of the protein, for monitoring
CC therapeutic effect during clinical trials and other treatment, as bait
CC proteins in a two-hybrid or three-hybrid assay, and in pharmacogenomic
CC analysis. The proteins and nucleic acids encoding them are useful for
CC diagnosis and treatment of disorders selected from disorders of the
CC spleen, lung such as Alzheimer's gyndrome, liver such as viral
CC hepatitis, brain such as Alzheimer's disease, haematopoietic stem cells
CC cliscase, colon such as Crohn's disease, hernic puch as such as get's
CC disease, colon such as Crohn's disease, uterus and endometrium such as
CC disease, colon such as actinic keratosis, disorders of the heart
CC such as myocarditis, disorders such as systemic lupus erythematosus,
CC disorders involving the thymus such as DiGeorge syndrome,
CC disorders involving the thymus such as DiGeorge syndrome,
CC disorders involving such as peripheral B-cell neoplasms,
CC disorders and epididymis such as teratoma. Numerous examples of
CC each type of disorder are given in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 1080;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1729 BP; 461 A; 403 C; 302 G; 563 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-432880/46.
P-PSDB; AAU04584.
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Sequence 1
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G-protein coupled receptors purinoreceptor 1 (p2y1) Patent: EP 1219638-A 1 03-JU
                                                  human.
Homo sapiens
                                      Bukaryota; Metazoa;
Mammalia; Eutheria;
                       Fidock, M.D.
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Patent EP1219638
                                      Chordata;
Primates;
 03-JUL-2002
              having homology
                                      Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                        AGGGTCATTCGGATCGAATCTCGCCTGCTTTCAATCAGTTGTTCCATTGAGAATCAGATC
                                                                                                      AGGCTAACCATTCTGCTACTCCCTTGCATTTTACGTATGTTTTTTACCCCTTCCATATCTTG
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CTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGATGCAAA
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/db_xref="taxon:9606"
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Pred. No. 6.9e-253;
0; Mismatches 1;
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TITLE
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                                                                                      GGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTTTC
                                                                                                                                                    Submitted (10-APR-2002) Shigeki Takeda, Gunma University, Department of Biological and Chemical, Engineering, Faculty Engineering; 1-5-1, Kiryu, Gunma 376-8515, Japan (E-mail:stakeda@bce.gunma-u.ac.jp, Tel:+81-277-30-1434,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 1014)
Takeda,S., Kadowaki,S.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax:+81-277-30-1434)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome sequence
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Identification of G protein-coupled receptor genes from the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
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/product="putative G-protein coupled receptor"
/protein_id="mah89311.1"
/protein_id="mah89311.1"
/db_xref="gi:20152260"
/translation="mnepldyLanasDFPDYAAAFGNCTDENIPLKMHYLFVIYGIIF
/translation="mnepldyLanasDFPDYAAAFGNCTDLLYLTSLEPILHYYASGENMIFG
DFMCKFIRESFHFNLYSSILFLTCFSIFRYCVIIHPMSCPSIHKTRCAVVACAVWAII
SLVAVIPMTFLITSTMRTNRSACLDLTSSDELMTIKWYMLILTATTFCLFLVIVTLCY
TTIIHTLTHGLQTDSCLKQKARRLTILLLLAFYVCFLPFHILRVIRIESRLLSISCSI
ENQIHEAYIVSRPLAALNTFGNLLLYVVVSDNFQQAVCSTVRCKVSGNLEQAKKISYS
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                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1014)

Lee, D.K., Nguyen, T., Lynch, K.R., Cheng, R., Vanti, W.B., Arkhitko, O., Lewis, T., Evans, J.F., George, S.R. and O'Dowd, B.F.

Discovery and mapping of ten novel G protein-coupled receptor genes Gene 275 (1), 83-91 (2001)
 2 (bases 1 to 1014)
Lee, D.K., Nguyen, T.,
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 Nguyen, T., Lynch, K.R.,
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Cheng, R.,
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Sequence
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1014)
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Sequence 1 from Patent W00187980
AX379468
                                                                                                                                                                                                                                                                                                                                                                       encoding human gpcr proteins, and uses thereof Patent: WO 0187980-A 1 22-NOV-2001;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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Beasley,E.M.
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                                Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1729)
Glucksmann,M.A. and White,D.
                                                                                                         Sequence 2:
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         26904, 38911, and 39404, seven-transmembrane coupled receptors
Patent: WO 0149847-A 2 12-JUL-2001;
   Millennium Pharmaceuticals,
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                                                          Craniata; Vertebrata;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 67645)
Submitted (27-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                   Skuce, C
                                                                                                                                                               complete sequence.
AL356486
AL356486.12 GI:15
                                                                                                                                                                                                            AL356486 67645 b
Human DNA sequence from clone
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                                    Direct Submission
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP better.
TGACCAGCCTCCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAACTGGGATCTTTGGAG
                                                                                                                              GACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATCTGCTGTATC
                                                                                                                                                                                 TCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTTTCAAAATGA
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RR11-721F14 is from the library RPCI-11.3 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RPI1-721F14 It may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true left end of clone RPI1-199B17 is at 65646 in this sequence. The true right end of clone RPI1-65L19 is at 2000 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at http://www.sanger.ac.uk/NGD/Chrophara
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On Sep 28, 2001 this sequence version replaced gi:15787734.
During sequence assembly data is compared from overlapping clones.
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/chromosome="13"
/clone="RP11-721F14"
/clone=lib="RPCI-11.3"
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be approximately 110bp by restriction digest data."
13252 c 13216 g 20635 t
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                              CTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCTATACCACGATTATCC
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CTGCAACTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCTATACCACGATTATCC
                                                                                                     GTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAACCTGATTTTGA
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Patent: WO 0246414-A 1 13-JUN-2002;
Bristol-Myers Squibb Company (US)
Location/Qualifiers
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                                                                                                                                        AL Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST); 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan (E-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/, Tel:81-3-359-8080, Fax:81-3-3599-8081)
This sequence is a seven transmembrane helix receptor candidate predicted from the whole human genome sequences using our automated system that contains programs of gene finding (Genebecoder), sequence search, motif-domain assignment and transmembrane helix prediction.
And the sequence is submitted by the collaborative project between [Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST)] and [Genome Science Division, Research Center for Advanced Science and
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Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                         Science Division, Research Center for Advanced Technology (RCAST), University of Tokyo].

Location/Qualifiers
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